

FIG. I

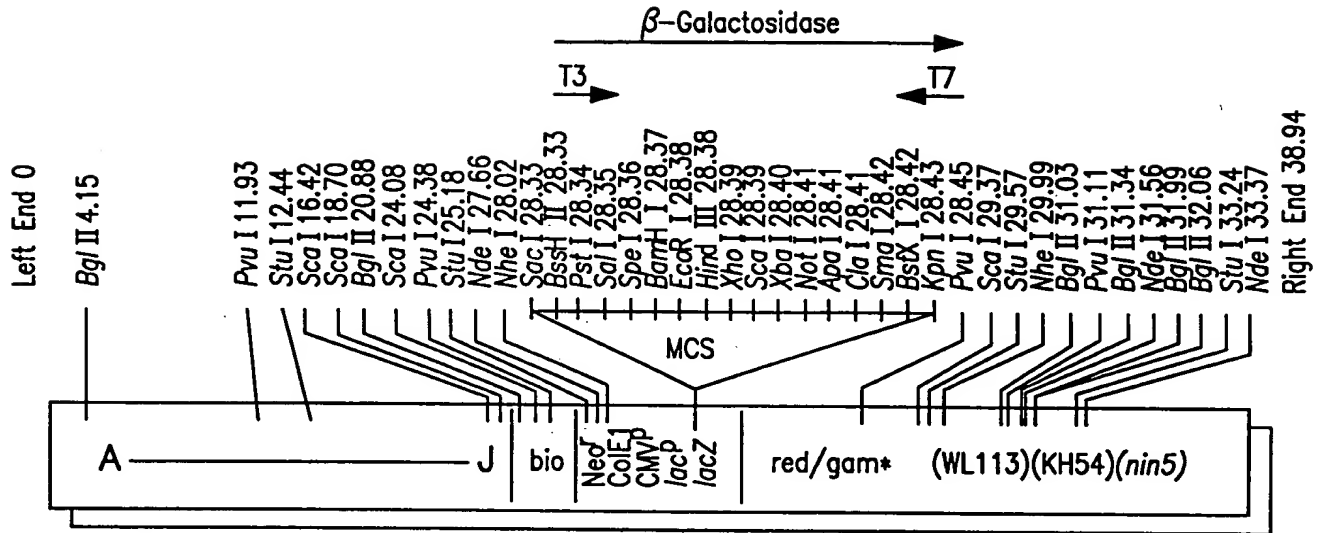


FIG. 2A

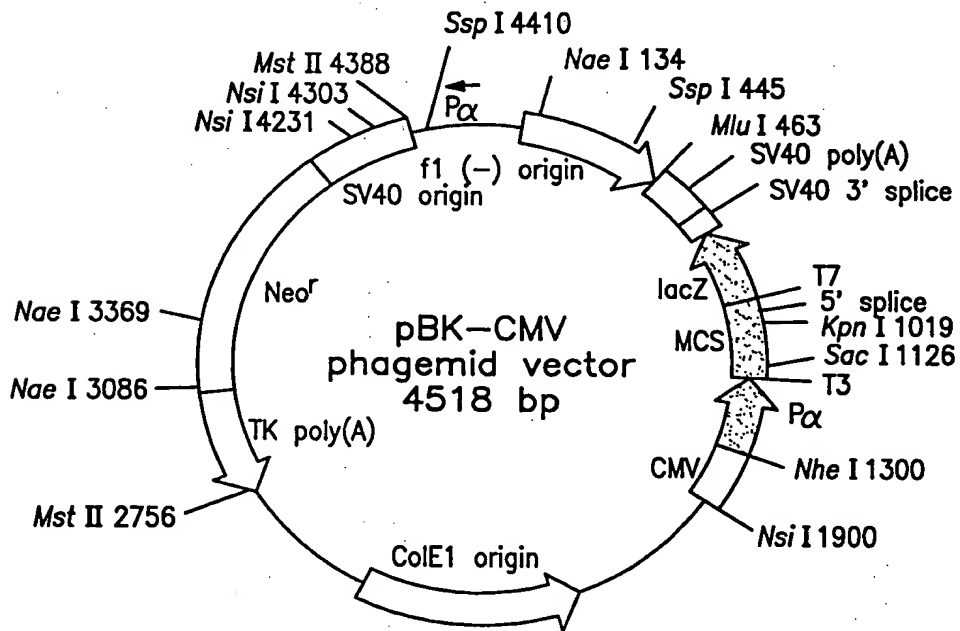


FIG. 2B

QC-RT-PCR primers for the 5' coding sequence of
Candida tropicalis 20336 P450CYP52A5A

5'	ATGATTGAACAACCTCCTAGAAATATTGGTAT	GTCGTTGTGCCAGTGTGTGTACATCATCAAA	CAACTCCTTGCATACACAAAAGACTCGCGTC	3'	90
3'	TACTAACTTGTGAGGATCTTATAACCAT	CAGCAACACGGTCACAACATGTAGTAGTTT	GTTGAGGAACGTATGTGTCTTGAGCGCAG	5'	
5'	TTGATGAAAAAGTTGGGTGCTGCCAGTC	ACAAACAAGTTGTACGACAACGGTTTCGGT	ATCGTCAATGGATGGAAGGCTCTCCAGTTC	3'	180
3'	AACACTTTTTCACCCACGACGAGGTCAG	TGTTTGTTCACATGCTGTTCGGAAGCCA	TAGCAGTTACCTACCTTCCGAGAGGTCAG	5'	
5'	Forward Primer 7581-97F			3'	270
3'	AAGAAGAGAGGGCAGGGCTCAAGAGTACAAC	GATTACAAGTTTGACCACTCCAGAACC	AGCGTGGGCACCTACGTACGTATCTTTTC	5'	
5'	TTCTTTCTCCCGTCCCGAGTTCTCATGTTG	CTAATGTTCAAACTGGTGAGGTTCTTGGGT	TCCGACCCCGTGGATGCAGTCATAAGAAAG	3'	360
3'	GGCACGAGGATCGTCGACCAAGATCCA	GAGAAATATCAAAAGCTATTTTGGCAACCCAG	TTTGGTGATTTTCTTTTGGGCAAGAGGCAC	5'	
5'	CCGTGGTCCTAGCAGCACTGGTTTCTAGGT	CTCTTATAGTTTCGATAAAACCGTTGGGTC	AAACCACTAAAGAAACCCGTTCTCCGTC	3'	450
3'	ACTCTTTTAAAGCCTTTGTTAGGTGATGGG	ATCTTCACATTGGACGGCGAAGGCTGGAAG	CACAGCAGAGCCATGTTGAGACCAACAGTTT	5'	
5'	TGAGAAAAATTCGGAAACAATC	CACTACCC	TAGAAGTGTAACTTCCGCTTCCGACCTTC	3'	540
3'	Reverse Primer 7581-97R			5'	
5'	GCCAGAGAAACAAGTTGCTCATGTGACGTCG	TTGGAACCAACACTTCCAGTTGTTGAAGAAG	CATATTCTTAAGCACAAGGGTGAATACCTTT	3'	
3'	CGGTCTCTTGTTCACGAGTACACTGCAGC	AACCTTGGTGTGAAGGTCAACAACCTTCTTC	GTATAAGAATTGCGTGTCCCACTTATGAAA	5'	

FIG. 3

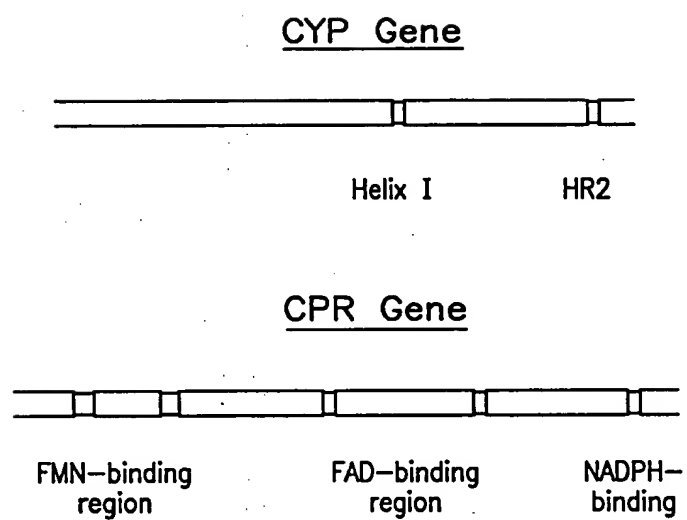


FIG. 4

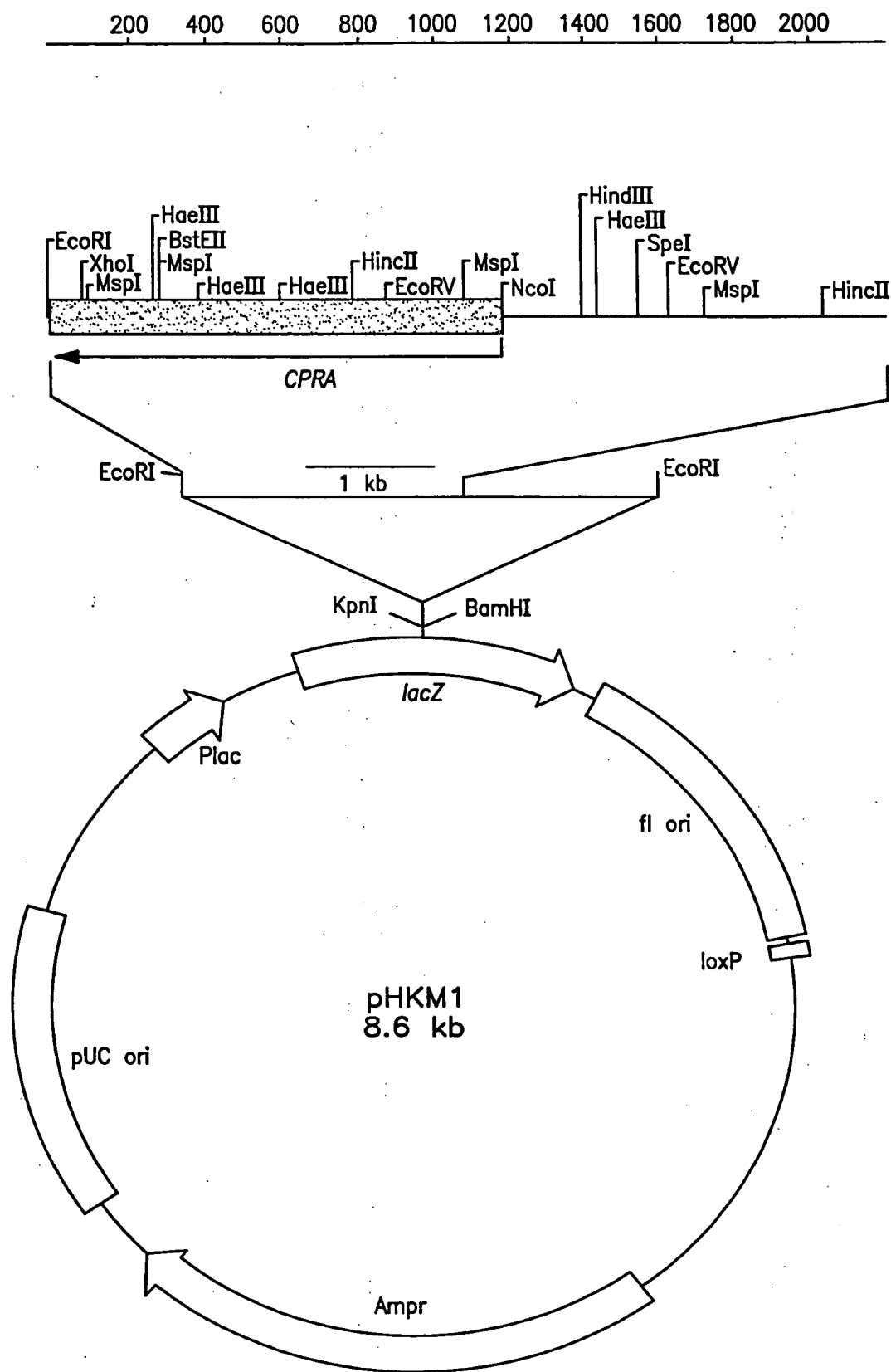


FIG. 5

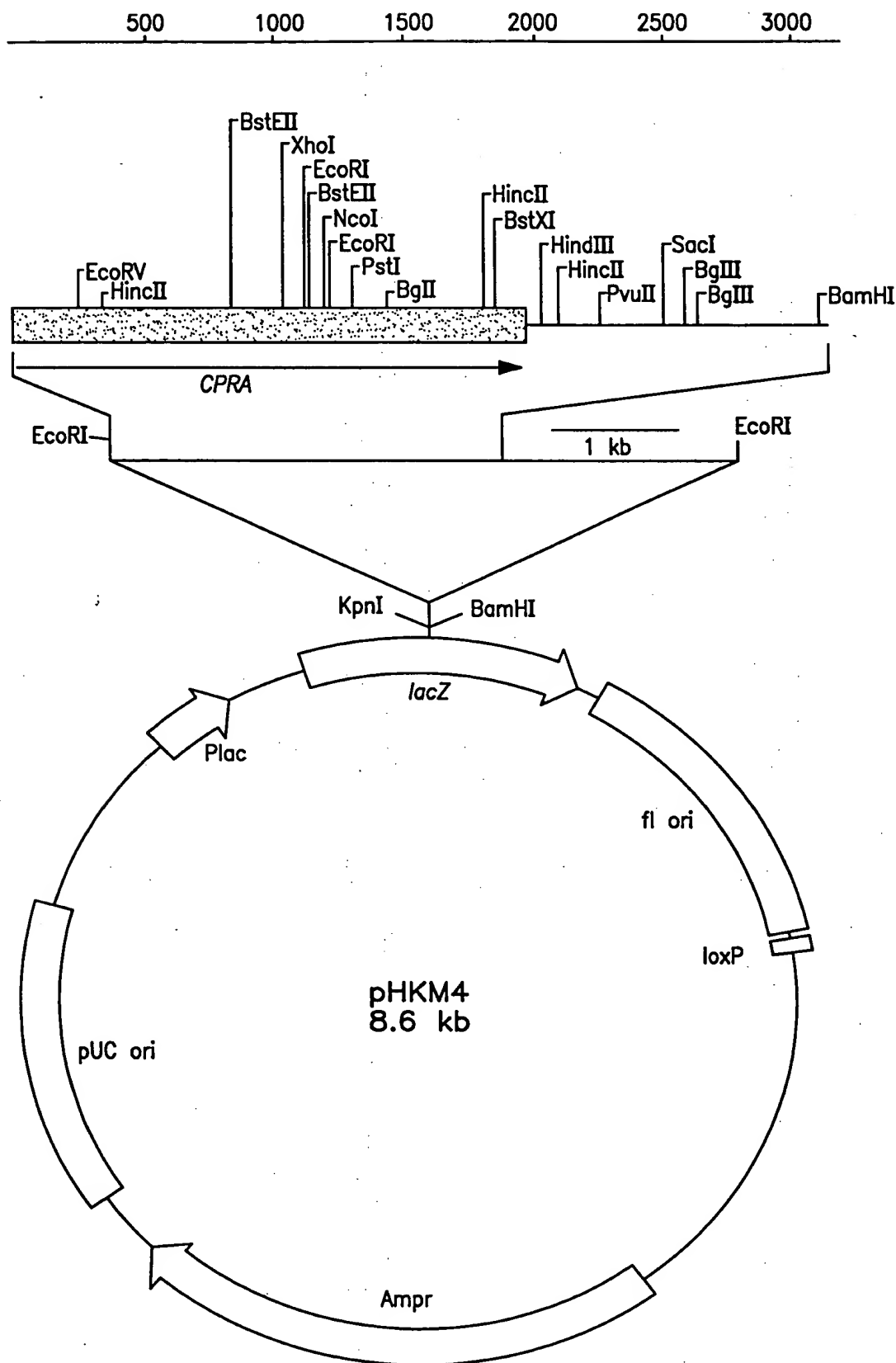


FIG. 6

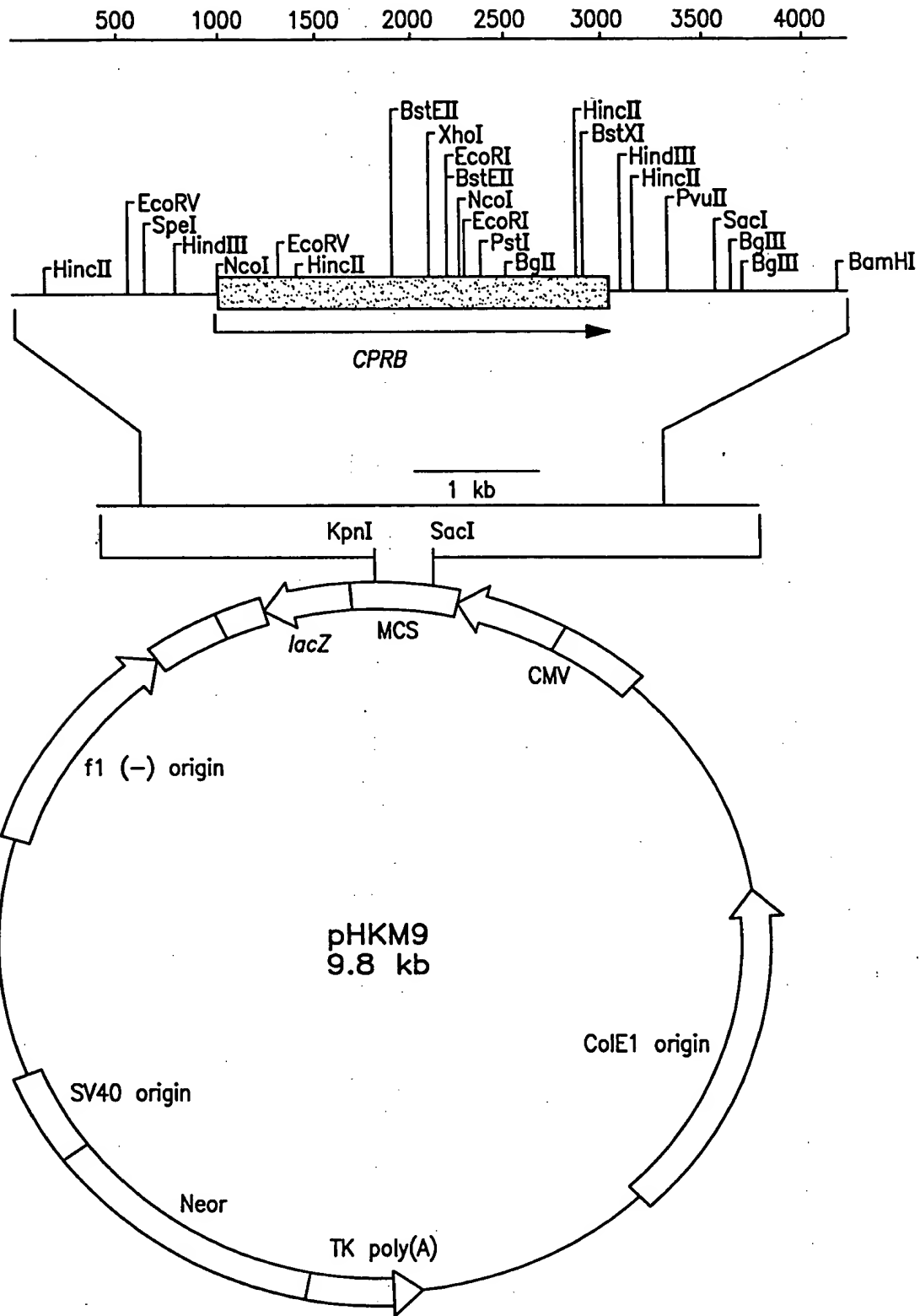


FIG. 7

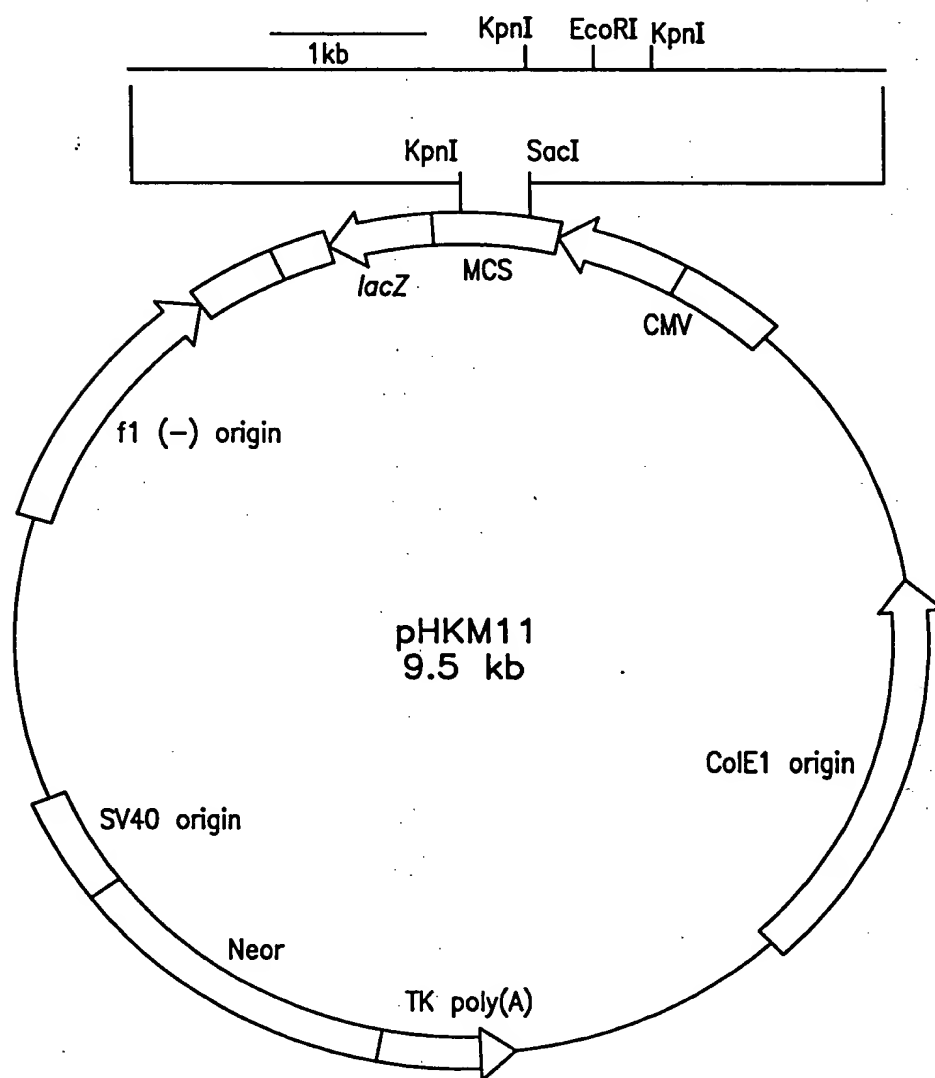
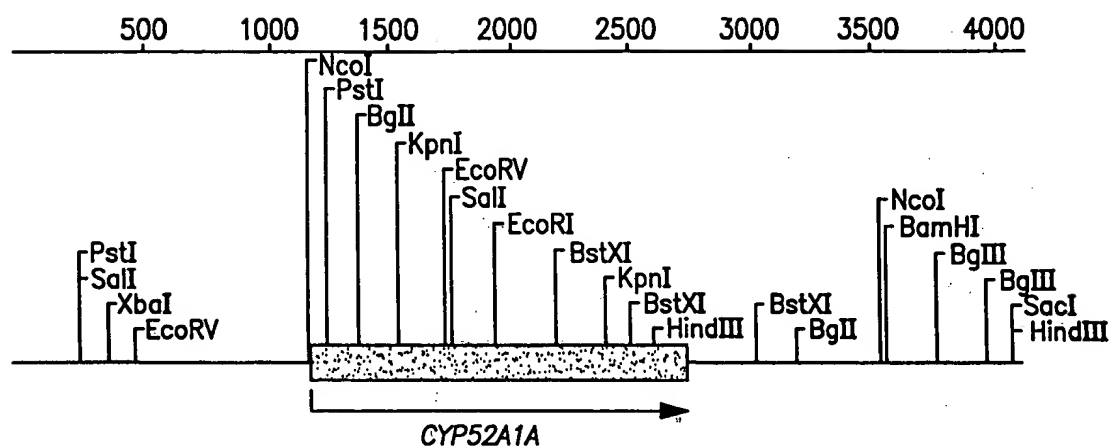


FIG. 8

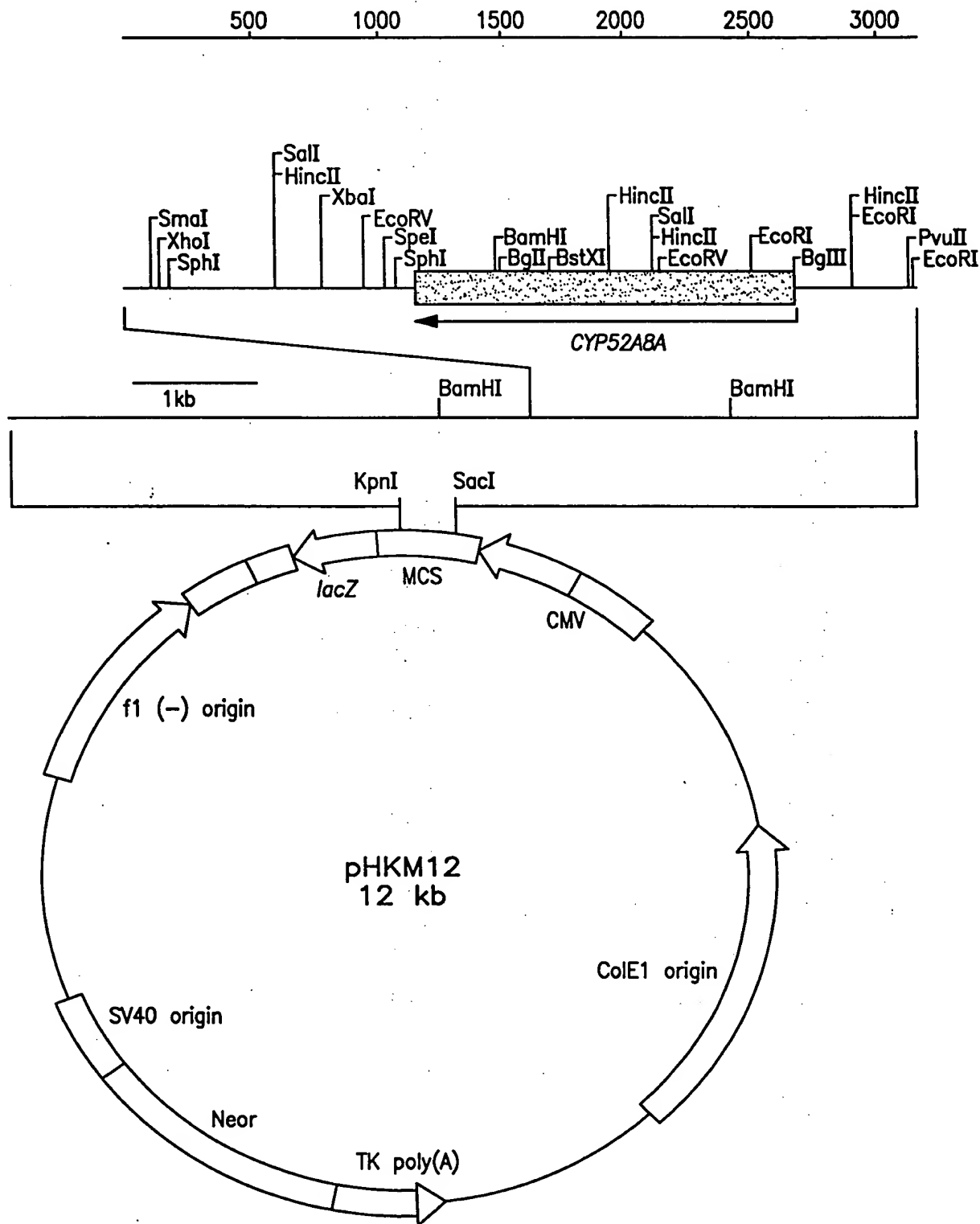


FIG. 9

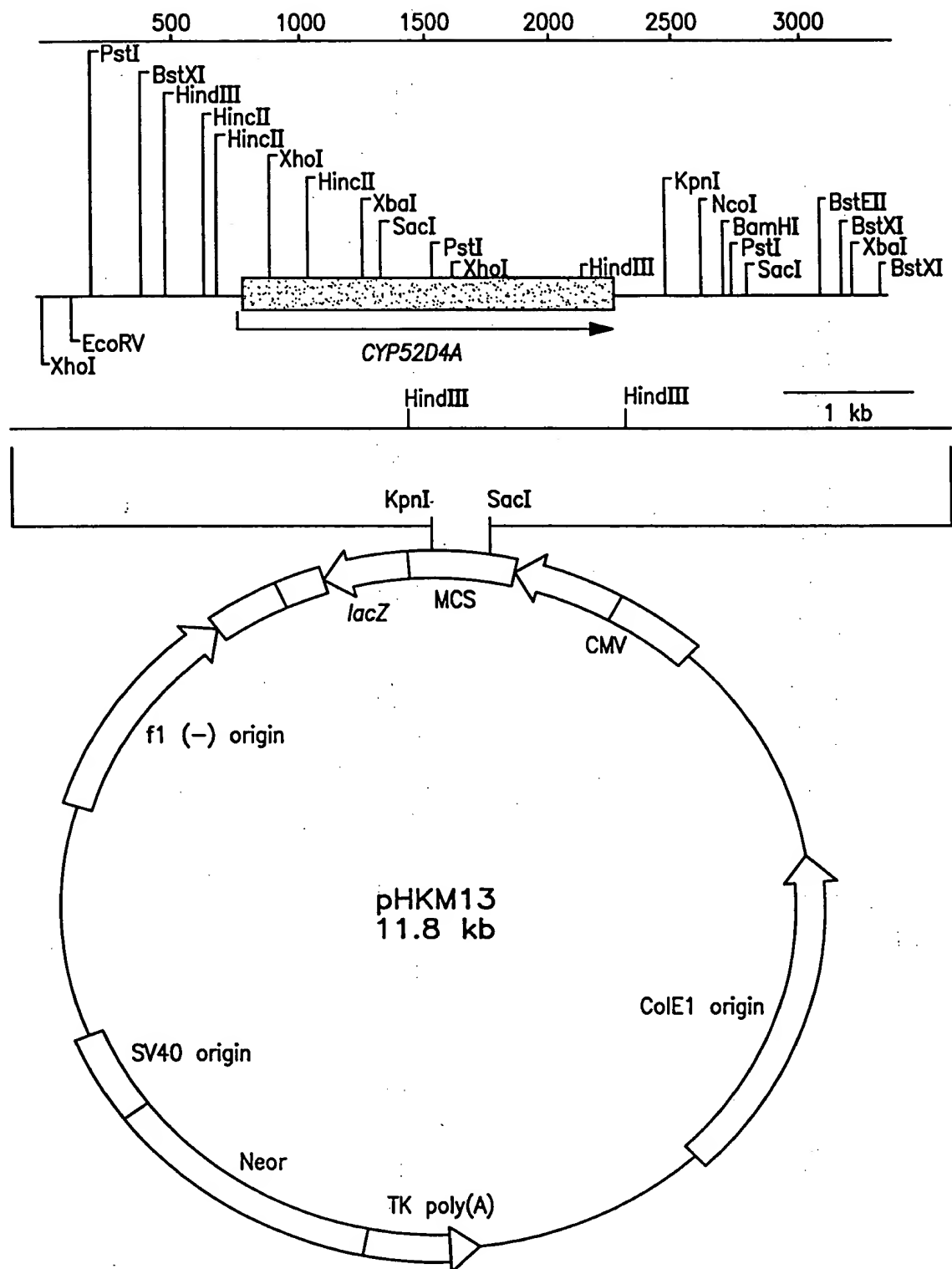


FIG. 10

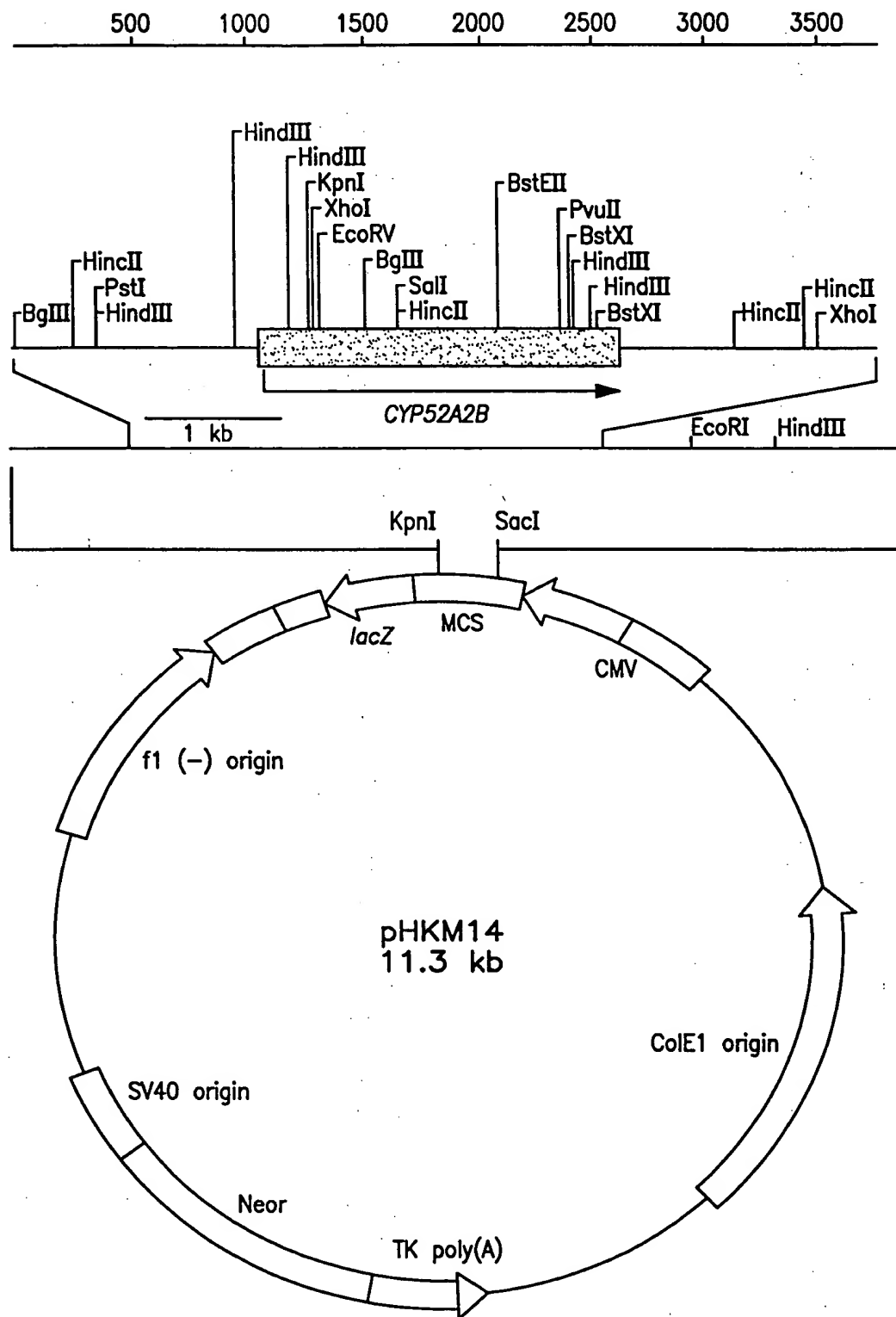


FIG. 11

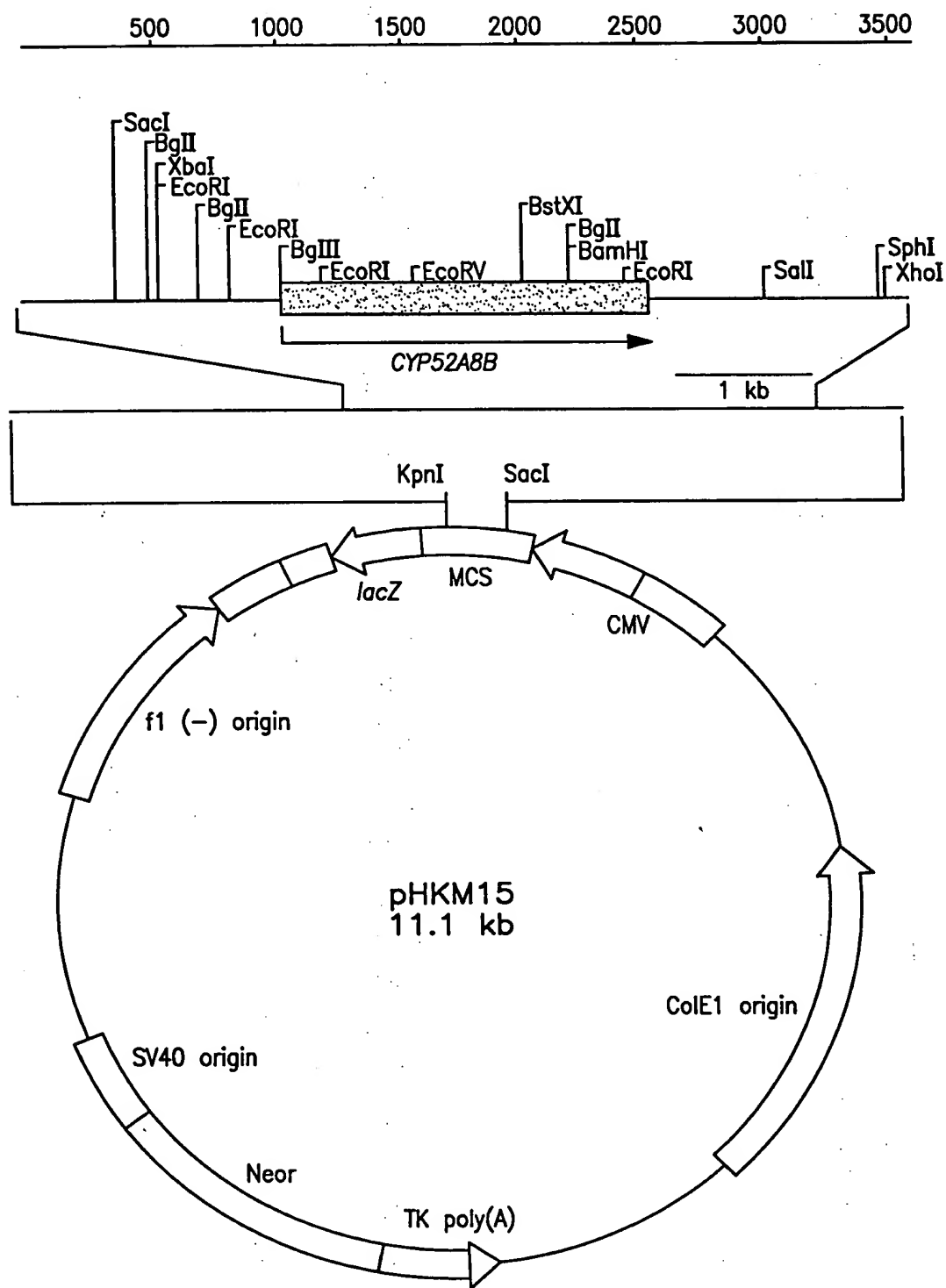


FIG. 12

C. tropicalis 20336 CPR Allele DNA Alignment of DS Sequence

CPRB	1	TATATGATATATATATCTTCCTGTGTAATTATTATTTCGTATTTCGTTAATACTTACTACATTTTTTT	CATCA	5
CPRB	1			70
CPRB	1		*	
CPRB	6	AGATCATCTATGGGATAATTA-----CGACAGCAACATTGCAGAAAAGCGTTGGTCACAATCGAAAGA		70
CPRB	71	TCCTTTATTTATGAAGAAAAGGAGAGTTCGTAAGTTGAGTTGAGTAGAATAGGCTGTGTGTCATACGGGGA		140
CPRB		* ** **** ** ** *	*** * *	**
CPRB			** ** *	**
CPRB	71	GCCTATG-GCGTTGCCGTCGTTGAGGCAAAATGACAGCAC--CAACAATAACGATGTTGCCAGTGAAGAGC		137
CPRB	141	GCAGAGGAGAGTATCCGACGAGGAGAACTGGGTGAAATTTTCATCTATGCTGTGCGTCCCTGTACTGTAC		210
CPRB		** * * * *	** ** *	*
CPRB		** * * * *	** ** *	*
CPRB		** * * * *	** ** *	*
CPRB	138	CTTCAGAAACAGTCCATTGTTGACGCT--TAAGGCACGGATAATTACGTGGGGCAAGAACGCGGAATTA		205
CPRB	211	TGTAATCTTAGATTTCCTAGAGGTTGTTCTAGCAATAAAGTGTTCAGAGATACAATTTTACAGGCAAG		280
CPRB		* * * * *	* * *	*
CPRB		* * * * *	* * *	*
CPRB	206	GTTATGGGGGATCAAA--AGCGGAAGATTGTGTGCTTGTGGGTTTTTTCCTTTATTTTTCATATGAT		273
CPRB	281	GGTAAAGGATCAACTGATTAGCGGAAGATTGGTGTGCTGTGGGTTCTT--TTATTTTTCATATGAT		347
CPRB		* ** ** *	***** ** *	*****
CPRB		* ** ** *	***** ** *	*****
CPRB	274	TTCTTTGCGCAAGTAACATGTGCCAATTTAGTTTGTGATTAGCGTGCC-CCACAATTGGCATCGTGGACG		342
CPRB	348	TTCTTTGCGCGAGTAACATGTGCCAATCTAGTTTATGATTAGCGTACCTCCACAATTGGCATCTTGGACG		417
CPRB		*****	***** **	*****
CPRB		*****	***** **	*****
CPRB	343	GGCGTGTTTTGTGATACCCCAAGTCTTAACTAGCTCCACAGTCTCGACGGTGTCTCGACGATGTCTTCTT		412
CPRB	418	GGCGTGTTTTGTGATACCCCAAGCCTTATTTAGTTCCACAGTCTCGACGGTGTCTCGCCGATGTCTTCTC		487
CPRB		*****	***** **	*****
CPRB		*****	***** **	*****

FIG. 13A-I

CPRA	413	CCACCCCTCCCATGAATCAATCAAGTTGTTGGGGGATCTCCCAAGGGCACCGGAGTTAATGCTTATG	482
CPRB	488	CCACCCCTCGCAGGAATCATTCGAAGTTGTTGGGGGATCTCCTCC-----GCAGTTTATGTTTCATG	548
		***** ** ***** ** ***** ***** ** * ***** ** * ** *	
CPRA	483	TTTTCTCCCACTTTGGTTGTGATTGGGGTAGTCTAGTGAGTTGGAGATTTTCTTTTTTTTCGCAGGTGTCTC	552
CPRB	549	TCTTTCCCACTTTGGTTGTGATTGGGGTAGCGTAGTGAGTTGGTGATTTTCTTTTTT-CGCAGGTGTCTC	617
		* * ***** ***** ***** ***** ***** ***** ***** ***** *****	
CPRA	553	CGATATCGAAATTTGATGAATATAGAGAGAAGCCAGATCAGCACAGTAGATTGCCCTTTGTAGTTAGAGAT	622
CPRB	618	CGATATCGAAGTTTGATGAATATAG---GAGCCAGATCAGCATGGTATATTGCCCTTTGTAGATAGAGAT	683
		***** ***** ***** ***** ***** ***** ***** ***** *****	
CPRA	623	GTTGAACAGCAACTAGTTGAATTACCGCCACCACCTTGACAGCAAGTGCAGTGAGCTGTAAACGATGCAG	692
CPRB	684	GTTGAACAACAACACTAGCTGAATTACACACCCACCGCT-----AAACGATGCCG	730
		***** ***** ***** ***** ***** ***** ***** ***** *****	
CPRA	693	CCAGAGTGTCAACCACTGACCGTTGGGTGGAGTTGTTGTTGTTGGCAGGGCCATATTGCTAA	762
CPRB	731	ACAGGTGTCAACCGCCAACTGACCGTTGGGTGGAGTTG-----TTGTTGGCAGGGCCATATTGCTAA	791
		*** ***** ***** ***** ***** ***** ***** ***** *****	
CPRA	763	ACGAAGACAAGTAGCACAAAACCCAAAGCTTAAGAACAAAAATAAAAAAATTCATACGACAATTCCAAAG	832
CPRB	792	ACGAAGAGAAGTAGCACAAAACCCAAAGTTAAGAACAA---TTAAAAAAAATTCATACGACAATTCCACAG	858
		***** ***** ***** ***** ***** ***** ***** ***** *****	
CPRA	833	CCATTGATTACATAAT--CAACAG-TAAGACAGAAAAAACTTTCAACATTTCAAAGTTCCCTTTTTCCT	899
CPRB	859	CCATTTACATAATCAACAGCGACAAATGAGACAGAAAAAACTTTCAACATTTCAAAGTTCCCTTTTTCCT	928
		***** * ** * ** * ***** ***** ***** ***** ***** ***** *****	

FIG. 13A-2

[illegible]

FIG. 13A-3

[illegible]

FIG. 13B-1

CPRA	1523	AAGGTGGTGACAGGTTTGTCTGAATACCGCTGAAGTGATGACGGTACTGGCACCTTGGACGAAGATTTCAT	1592
CPRB	1550	AAGGTGGTGACAGATTGTCTGAATATGCTGAAGTGACGACGGCACTGGCACCTTGGACGAAGATTTCAT	1619
		*****	*****
CPRA	1593	GGCCTGGAAGGACAAATGTCTTTGACGCCTTGAAGAAATGAATTGAACTTTGAAGAAAAGGAATTGAAGTAC	1662
CPRB	1620	GGCCTGGAAGGATAAATGTCTTTGACGCCTTGAAGAAATGAATTGAACTTTGAAGAAAAGGAATTGAAGTAC	1689
		*****	*****
CPRA	1663	GAACCAAAACGTGAAATTGACTGAGAGAGACGACTTGTCTGTCTGCTGACTCCCAAGTTTCCTTGGGTGAGC	1732
CPRB	1690	GAACCAAAACGTGAAATTGACTGAGAGAGATGACTTGTCTGTCTGCCGACTCCCAAGTTTCCTTGGGTGAGC	1759
		*****	*****
CPRA	1733	CAAAACAAGAAGTACATCAACTCCGAGGGCATCGACTTGACCAAGGGTCCATTTCGACCACACCCACCCATA	1802
CPRB	1760	CAAAACAAGAAGTACATCAACTCCGAGGGCATCGACTTGACCAAGGGTCCATTTCGACCACACCCACCCATA	1829
		*****	*****
CPRA	1803	CTTGGCCAGAAATCACCGAGACGAGAGAGTTGTTTCAGCTTCCAAGGACAGACACTGTATCCACGTTGAATTT	1872
CPRB	1830	CTTGGCCAGGATCACCGAGACGAGAGAGTTGTTTCAGCTTCCAAGGAAAGACACTGTATTTCACGTTGAATTT	1899
		*****	*****
CPRA	1873	GACATTTCTGAATCGAACTTGAAATACACCACCGGTGACCATCTAGCTATCTGGCCATCCAACTCCGACG	1942
CPRB	1900	GACATTTCTGAATCGAACTTGAAATACACCACCGGTGACCATCTAGCCATCTGGCCATCCAACTCCGACG	1969
		*****	*****
CPRA	1943	AAAACATTAAGCAATTTGCCAAGTGTTCGGATTGGAAGATAAACTCGACACTGTTATTGAATTGAAGGC	2012
CPRB	1970	AAAACATCAAGCAATTTGCCAAGTGTTCGGATTGGAAGATAAACTCGACACTGTTATTGAATTGAAGGC	2038
		*****	*****

FIG. 13B-2

Cpra	2013	GTTGGACTCCACTTACACCATCCCATTCCCCAACCCCAATTACCTACGGTGCTGTTCATTAGACACCATTTA	2082
CPRB	2040	ATTGGACTCCACTTACACCATTCCATTCCCAACTCCAATTACTTACGGTGCTGTTCATTAGACACCATTTA	2109

Cpra	2083	GAAATCTCCGGTCCAGTCTCGAGACAATCTTTTTTGTGTCATTTGCTGGGTTTGCTCCTGATGAAGAAAACAA	2152
CPRB	2110	GAAATCTCCGGTCCAGTCTCGAGACAATCTTTTTTGTGTCGATTGCTGGGTTTGCTCCTGATGAAGAAAACAA	2179

Cpra	2153	AGAAGGCTTTTACCAGACTTGGTGTGACAAAGCAAGAAATTCGCCGCCAAGGTCA CCGCAGAAAAGTTCAA	2222
CPRB	2180	AGAAGACTTTTACCAGACTTGGTGTGACAAACAAGAAATTCGCCACC AAGGTTACCGCAGAAAAGTTCAA	2249

FIG. 13B-3

CPRB	2223	CATTGCCGATGCCCTTGTTATATTCCTCCAACAACGCTCCATGGTCCGATGTTCCCTTTTGAATTCCCTTATT	2292
CPRB	2250	CATTGCCGATGCCCTTGTTATATTCCTCCAACAACACTCCATGGTCCGATGTTCCCTTTTGAATTCCCTTATT	2319

CPRB	2293	GAAAAAGTTCCACACTTGACTCCACGTTACTACTCCATTTCTGTTCTTCGTCATTGAGTGAAAAAGCAACTCA	2362
CPRB	2320	GAAAAACATCCAACACTTGACTCCACGTTACTACTCCATTTCTTCTTCGTCGTTGAGTGAAAAAACAACACTCA	2389

CPRB	2363	TCAACGTTACTGCAGTTGTTGAAGCCGAAGAAGCTGATGGCAGACCAGTCACTGGTGTGTGTACACCAA	2432
CPRB	2390	TCAATGTTACTGCAGTCGTTGAGGCCGGAAGAAGCCGATGGCAGACCAGTCACTGGTGTGTGTACACCAA	2459

CPRB	2433	CTTGTGAAGAACGTTGAAATTTGTGCAAAAACAAGACTGGCGAAAAGCCACTTGTCCACTACGATTGTGAGC	2502
CPRB	2460	CTTGTGAAGAACATTTGAAATTTGCGCAAAAACAAGACTGGCGAAAAGCCACTTGTTCACACTACGATTGTGAGC	2529

CPRB	2503	GGCCCAAGAGGCAAGTTCAACAAGTTCAAGTTGCCAGTGCAATGTGAGAAAGATCCAACTTTAAGTTGCCAA	2572
CPRB	2530	GGCCCAAGAGGCAAGTTCAACAAGTTCAAGTTGCCAGTGCAATGTGAGAAAGATCCAACTTTAAGTTGCCAA	2599

CPRB	2573	AGAACTCCACCCAGTTATCTTGATTGGTCCAGGTACTGGTGTGCCCCCATTTGAGAGGTTTGTGTCAG	2642
CPRB	2600	AGAACTCCACCCAGTTATCTTGATTGGTCCAGGTACTGGTGTGCCCCCATTTGAGAGGTTTGTGTCAG	2669

CPRB	2643	AGAAAAGAGTTCAACAAGTCAAGAATGGTGTCAATGTTGCCAAGACTTTGTTGTTTATGTTGCAGAAAC	2712
CPRB	2670	AGAAAAGAGTTCAACAAGTCAAGAATGGTGTCAATGTTGCCAAGACTTTGTTGTTTATGTTGCAGAAAC	2739

FIG. 13C-1

Cpra	3203	TAACTATTATCTACTCGTCTACTTCTTTGGCATTGACATCAACATTACCGTTCCCATTAACCGTTGCCGTT	3272
CPRB	3216	TAATTATTATCTACTCGTCTACTTCTTTGGCATTGGCATTGGCATTGGCATTGCCGTTGCCGTT	3285
		*** ****	
Cpra	3273	GGCAATGCCGGGATAATTAGTACAGTATCTCCAATCCGGATTTGAGCTATTGTAGATCAGCTGCAAGTCA	3342
CPRB	3286	GGTAATGCCGGGATAATTAGTACAGTATCTCCAATCCGGATTTGAGCTATTGTAAAATCAGCTGCAAGTCA	3355
		** *****	
Cpra	3343	TTCTCCACCCTCAACCAGTACTTATACCTTCATCTTTGACTTCAAGTCCCAAGTCATAAATATTACAAGTTA	3214
CPRB	3356	TTCTCCACCCTCAACCAGTACTTATACCTTCATCTTTGACTTCAAGTCCCAAGTCATAAATATTACAAGTTA	3425

FIG. 13C-3

CPRB	3903	CTCCTGGTTCCTCTCATAGTACAACTGGCACTTCTTCGAGAGGCTCAATTCCCTCGTAGTTCCTCCGTCCTCAAG	3972
CPRB	3916	CTCCTGGTTCCTTTCATAGTACAACTGGCATTTCTTCGAGAGACTCAACTCCTCGTAGTTCCTCCGTCCTCAAG	3985

CPRB	3973	ATATTCGGCAACAAGAGCCCCGTACCGCTCACGGAGCATCAAGTCGTGGCCCTGGTTGTTCAACTTGTGTA	4042
CPRB	3986	ATATTCGGCAACAAGAGCCCCGTACCGCTCACGGAGCATCAAGTCGTGGCCCTGGTTGTTCAACTTGTGTA	4055

CPRB	4043	TGAAGTCCGAGGTCAAGACAATCAACTGGATGTCGATGATCTGGTGGGGAACAAGTTCCTTGCATTTTAG	4112
CPRB	4056	TGAAGTCCGATGTCAAGACAATCAACTGGATGTCGATGATCTGGTGGGGAACAAGTTCCTTGCATTTTAG	4125

CPRB	4113	CTCGATGAAGTCGTACAACTCACACGTCGAGATATACTCCTGTTCCTTCAAGAGCCGGATCCGCAAG	4182
CPRB	4126	CTCGATGAAGTCGTACAACT	4125

CPRB	4183	AGCTTGTGCTTCAAGTAGTCGTTG	4206
CPRB	4146		4145

FIG. 13D-2

CPRB	MALDKLDLYVITLVAAYFAKNQFLDQPDGTGFLNTDSCNSRDVLLTLKNNKNTL	60
CPRB	MALDKLDLYVITLVAAYFAKNQFLDQPDGTGFLNTDSCNSRDVLLTLKNNKNTL	60
CPRB	LLFGSQTGTAEDYANKLSRELHSRFGGLKTMVADFADYDWDNFGDITEDILVFFIVATYGE	120
CPRB	LLFGSQTGTAEDYANKLSRELHSRFGGLKTMVADFADYDWDNFGDITEDILVFFIVATYGE	120
CPRB	*	
CPRB	GEPTDNADEFHTWLTTEADTLSTLKYTVFGLGNSTYEFFNAIGRKFDRLILSEKGGDRFAE	180
CPRB	GEPTDNADEFHTWLTTEADTLSTLKYTVFGLGNSTYEFFNAIGRKFDRLILSEKGGDRFAE	180
CPRB	YAEGLDGTGLDEDFMAWKDNVFDALKNDLNFEKELKYEPNVKLTERDDLSAADSQVSL	240
CPRB	YAEGLDGTGLDEDFMAWKDNVFDALKNDLNFEKELKYEPNVKLTERDDLSAADSQVSL	240
CPRB	*	
CPRB	GEPNKKYINSEGIDLTGPFDPHTHPYLARITETRELFSSKDRHCHIVEFDISESNLKYTT	300
CPRB	GEPNKKYINSEGIDLTGPFDPHTHPYLARITETRELFSSKDRHCHIVEFDISESNLKYTT	300
CPRB	GDHLAIWPSNSDENIKQFAKCFGLEDKLDTVIELKALDSTYTIPTPTITYGAVIRHHLE	360
CPRB	GDHLAIWPSNSDENIKQFAKCFGLEDKLDTVIELKALDSTYTIPTPTITYGAVIRHHLE	360
CPRB	*	
CPRB	ISGPVSRQFFLSIAGFAPDEETKKAFTRLGGDKQEFKAKVTRRRKFNADALLYSSNNAPW	420
CPRB	ISGPVSRQFFLSIAGFAPDEETKKAFTRLGGDKQEFKAKVTRRRKFNADALLYSSNNAPW	420
CPRB	**	
CPRB	SDVPFEFLIENVPHTLTPRYYSISSSSLSEKQLINVTAVVEAEEDGRPVTGVVNTNLLKN	480
CPRB	SDVPFEFLIENVPHTLTPRYYSISSSSLSEKQLINVTAVVEAEEDGRPVTGVVNTNLLKN	480

FIG. 14A

	* *		
CPRA	VEIVQNTGEKPLVHYDLSGPRGKFNFKLPVHVRRSNFKLPKNSTTPVILIGPGTGVP	540	
CPRB	IEIAQNTGEKPLVHYDLSGPRGKFNFKLPVHVRRSNFKLPKNSTTPVILIGPGTGVP	540	
CPRA	LRGFVRERVQQVKNGVNVGKTLIFYGCRNSNEDFLYKQEWAEYASVLGENFEMFNFSRQ	600	
CPRB	LRGFVRERVQQVKNGVNVGKTLIFYGCRNSNEDFLYKQEWAEYASVLGENFEMFNFSRQ	600	
CPRA	DPSKKVYVQDKILENSQLVHELLTEGAIYVCGDASRMARDVQTTISKIVAKSREISEDK	660	
CPRB	DPSKKVYVQDKILENSQLVHELLTEGAIYVCGDASRMARDVQTTISKIVAKSREISEDK	660	
CPRA	AAELVSKWKVQNRYQEDVW	680	
CPRB	AAELVSKWKVQNRYQEDVW	680	

FIG. 14B

CYP52A1A	60	GAAACAAATGACAACTCCTGCGTAACTTGCATAATCTTGTCTGACTAATTGAAAACTCCGGACGAGTCA	129
CYP52A2A	141	CTTGTTCGGTCAACCAATCTTGGTGTGACCCCAATGAAGTACGCTCAACAAATTGTCTGACAAGATCTC	210
CYP52A2B	1	GCTCAACAAATTGTCTGACAAGATCTC	26
CYP52A3A	82	AAACTCTAGTATAATGGTGATAACTGGTTGCACTCTTGCCATAGGCATGAAAATAGGCCGTTATAGTACT	151
CYP52A3B	1		0
CYP52A5A	8	GCCAGACTTGCTCACTTTTGACTCCCTTCGAAACTCAAAGTACGTTCAGGCGGTGCTCAACGAAACGCTC	77
CYP52A5B	83	GCCAGACTTGCTCACTTTTGACTCTCTTAGAAGCTCAAAGTACGTTTCAGGCGGTGCTCAACGAAACGCTT	152
CYP52A8A	1		0
CYP52A8B	1	AAACCGGATACAAGAAGACAGTCAA	28
CYP52D4A	1		0
CYP52A1A	130	GACCTCCAGTCAAACGGACAGACAGACAAACACTTGGTGCATGTTTCATACCTACAGACATGTCAACGGG	199
CYP52A2A	211	GCAACACAAAGGCTAACGCCTGGTTGTTGAACACCCGGTTGGTTCTTCTGCTGTAGAGGTGGTAAG	280
CYP52A2B	27	GCAACACAAAGGCTAACGCCTGGTTGTTGAACACACTGGTTGGTTGGTTCTTCTGCTGTAGAGGTGGTAAG	96
CYP52A3A	152	ATATTTAATAAGCGTAGGAGTATAGGATGCATATGACCCGGTTTTCCTATATTTTAAAGATAATCTCTAGT	221
CYP52A3B	1	CCTGCAGA	8
CYP52A5A	78	CGTATCTACCCGGGGGTACCAACGAAACATGAAGACAG--CTACGTGCAACACGACGTTGCCACCGGAGG	145
CYP52A5B	153	CGTATCTACCCGGGGGTGCCACGAAACATGAAGACAG--CTACGTGCAACACGACGTTGCCCGGTGGAGG	220
CYP52A8A	1		0
CYP52A8B	29	CAAGAACGTTAATGTCAACAGGCGCCAAAGACGG--TTTGGCGGACTTGGAAGAATGTGGCATTTGC	96
CYP52D4A	1		0

FIG. 15A-2

CYP52A1A	200	TGTTAGACGCGGTTCTTGGCAAAGAC-AGGTGTTGGCATCTCGTACGATGGCAACTGCAGGAGGTGTCG	268
CYP52A2A	281	AGATGCTCATTTGAAGTACACCCAGAGCCATTTTGGACGCTATCCACTCTGGTGAATTGTCCAAGGTTGAAT	350
CYP52A2B	97	AGATGTTCAATTGAAGTACACCCAGAGCCATTTTGGACGCTATCCACTCTGGTGAATTGTCCAAGGTTGAAT	166
CYP52A3A	222	AAATTTTGTAATCTCAGTAGGATTTTCATCAAATTTTCGCAACCAATTTGCGGAAAAAATGATTCCTTTTAC	291
CYP52A3B	9	ATTTCGGCGCCGTCGACAGAGTAGCAGTTATGCAAGCATGTGATTGTGGTTTTTGCAACCTGTTTGCAC	78
CYP52A5A	146	AGGCA-AAGACGGCAAGGAACCTATCT-TGGTGCAGAAGGACAGTCCGTTGGGTTGATTACTATTGCCA	213
CYP52A5B	221	AGGCA-AAGACGGTAAGGAACCTATTT-TGGTGCAGAAGGGCCAGTCCGTTGGGTTGATTACTATTGCCA	288
CYP52A8A	1		0
CYP52A8B	97	CCATG-ATGTTTATGTTCTGGAGAGGT-TTTTCAAGGAATCGTCACTCTCCGCCACCCACAAGAACCACCA	164
CYP52D4A	1		0

FIG. 15A-3

CYP52A1A	269	ACTTCTCCTTTAGGCAATAGAAAAGACTAAGAGAAACAGCGTTTTTACAGGTTGCATTGGTTAATGTAGT	338
CYP52A2A	351	ACGAAACTTTCCCACTCTTCAACTTGAATGTCCAACTCCTGTCCAGGTGTCCCAAGTGAATCTTGAA	420
CYP52A2B	167	ACGAGACTTTCCCACTCTTCAACTTGAATGTCCAACTCCTGTCCCAAGTGTCCCAAGTGAATCTTGAA	236
CYP52A3A	292	GTCAAAAGCTGA-ATAGTGCAGTTTAAAGCACCTAAATCACATATACAGCCTCTAGATACGACAGAGAA	360
CYP52A3B	79	GACAAATGATCG-ACAGT-CGATT--ACGTAATCCATATTATTAGAGGGGTAAATAAAATAAATGGCA	144
CYP52A5A	214	CGCAGACGGACCCAGAGTATTTTGGGGCCGACGCTGGTGAGTTTAAGCCGGAGAGATGGTTTGATTCA--	281
CYP52A5B	289	CGCAGACGGACCCAGAGTATTTTGGGGCAGATGCTGGTGAGTTCAAAACCCGGAGAGATGGTTTGATTCA--	356
CYP52A8A	1		0
CYP52A8B	165	GTTAACGAGATCCATATTTCACAACCCACCGCAAGGTGACAATGCTCAACAACAACAGCAACAACAACA--	232
CYP52D4A	1		0
CYP52A1A	339	ATTTTTTTAGTCCCAGCATTCTGTGGGTGCTCTGGGTTTCTAGAATAGGAAATCACAGGAGAAATGCAAA	408
CYP52A2A	421	CCCAACCAAGGCTGGACCGG-AAGGTGTTGACTCCTTCAACAAGGAAATCAAGTCTTTGGCTGGTAAGT	489
CYP52A2B	237	CCCAACCAAGGCTGGACCG--AAGGTGTTGACTCCTTCAACAAGGAAATCAAGTCTTTGGCTGGTAAGT	304
CYP52A3A	361	GCTCTTTATGATCTGAAGAAGCATTAGAATAGCT--ACTATGAGCCACTATTGGTGTATATATTAGGGA	427
CYP52A3B	145	GCC---AGAAATTCAAAACATTTTGCAAAACAATGCAAAAGATGAGAAACTCCAACAGAAAAATAAAAAA	210
CYP52A5A	282	AGCATGAAGAACTTGGGGTGTAATACTTGCCGTTCAATGCTGGGCCACGGACTTGTCTGGGGCAGCAGT	351
CYP52A5B	357	AGCATGAAGAACTTGGGGGTGAAGTACTTGCCGTTCAATGCTGGGCCCCCGGACTTGTCTGGGGCAGCAGT	426
CYP52A8A	1		0
CYP52A8B	233	ACCCCCACAAGAACAGTGAATAATGCCAGTCAA-CAAAGAGTGGTGACAGACGAGGGAGAAAAACGCAAG	301
CYP52D4A	1		0

FIG. 15B-I

CYP52A1A	409	TTCAGATGGAAGAACAAAGAGATAAAAAACAAAAAAACTGAGTTTTCACCAATAGAAATGTTTG----	474
CYP52A2A	490	TTGCTGAAAAAC--TTCAAGACCTATGCTGACCAAGCTACCGCTGA--AGTGAGAGCTGCAGGTCCAGAAG	555
CYP52A2B	305	TTGCTGAAAAAC--TTCAAGACCTATGCTGACCAAGCTACCGCTGA--AGTTAGAGCTGCAGGTCCAGAAG	370
CYP52A3A	428	TTGGTGCAATTAAAGTACGTACTATAAACAGAGAAAAATACTTAACCAATTTCTGGTGTATACCTTAGTGG	497
CYP52A3B	211	ACTCCGCAGC--ACTCCGAACCAACAAACAATGGGGGGGCCAG--AATTATTGAC--TATT-----	267
CYP52A5A	352	ACACTTTGATTGAAGCGAGCTACTTGCTAGTCCGGTTGGCCCGACCTAC-CGGGCAATAGATTG----	416
CYP52A5B	427	ACACTTTGATTGAAGCGAGCTATTGCTAGTCAGGTTGGCGCAGACCTAC-CGGGTAATCGATTTG----	491
CYP52A8A	1		0
CYP52A8B	302	CAACAGTGGTTCTGATGCAAGATCAGCTACACCGCTTCATCAGGAAAAAGC-AGGAGCTCCCACCAC----	366
CYP52D4A	1	GATGTGGTGCTTGATTCTCGAGACACATCCTTGTGAGGTGCCATGAATCTGTACCTG-----	58
CYP52A1A	475	-ATGATATCATCCACTCGCTAAACGAATCATGTGGGTGATCTTCTCTTTAGTTTGGTCTATCATATAAAC	543
CYP52A2A	556	CTTAAAGATAATTTATTCAATTTTAGTTTGCCTATTTATTCTCATTACCCATC-ATCATTCAACACTAT	624
CYP52A2B	371	CTTAAAGATAATTTATTCACTATTTAGTTTGCCTATTTATTCTCATCACCCTATC-ATCATTCAACAATAT	439
CYP52A3A	498	-TGAGGGACCTTTTCTGAACATTCGGGTCAAACTTTTTTTTGGAGTGCAGATCGATTTTTCGTTTGTGT	556
CYP52A3B	268	----GTGACTTTTTTTTATTTTTTCCGTTAA--CTTTTCATTGCAGTGAAGTGT--GTTACACGGGGTGGT	329
CYP52A5A	417	-CAGCCAGGATCGGCGTACC-CACCAAGAAAGAAAGTCGTTGATCAACATGAGTGTGCCGACGGGGTGT	484
CYP52A5B	492	-CTGCCAGGGTCGGCGTACC-CACCAAGAAAGAAAGTCGTTGATCAATATGAGTGTGCCGATGGGGTGGT	559
CYP52A8A	1		0
CYP52A8B	367	-CATATGCCCATCACGAGCAACACAGCAGGTTAGTGTATAGTAGTCTGTAGTTAAGTCAATGCAATGTA	435
CYP52A4A	59	-TCTGTAAGCACAGGGAACCTGCTTCAACACCTTATTGTCATATTCTGTCTATTGCAAGCGTGTGCTGCAAC	127

FIG. 15B-2

CYP52A1A	544	ACATGAAAGTGAAATCCAAA-TACACTACACTCGGGTATTGTCTCTCGTTTACAGATGTCATTGTC	612
CYP52A2A	625	ATATAAAGTTACTTCGGA-----TATCATTTGTAATCGTGCGTGTGCAATTGGATGATTTGGAA	683
CYP52A2B	440	ATATAAAGTTATTTCGGAAC-TCATA---TATCATTTGTAATCGTGCGTGTGCAATTGGGTAATTTGAAA	505
CYP52A3A	567	AATAATAGTGAAACCTTTGTG-TAATAAATCTTCATGCAAGACTTGCATAATTCGAGCTTGGAGTTCACG	635
CYP52A3B	330	GATGGTGTGGTTTCTACAA-TGCAAGGGCACAGTTGAAGGTTCCACATAACGT-TGCACCATATCAAC	397
CYP52A5A	485	TGT--AAAGCTTTATAAGGA-TGTAACGGTAGATGGATAGTTGTGTAGGAGGAGCGGAGATAAATTAGAT	551
CYP52A5B	560	TGT--AAAGTTTACAAAGGA-TCTAGATGGATATGTA-AGGTGTGTAGGAGGAGCGGAGATAAATTAGAT	625
CYP52A8A	1		0
CYP52A8B	436	CCA--ATAAGACTATCCCTT-CTTACAACCAAGTTTCTGCCGCGCTGTCTGGCA-ACAGATGCTGGCC	501
CYP52D4A	128	GATATCTGCCAAGGTATATAGCAGAACGCTGCTGATGGTTCTCTCCGGTCATATCTGTGGTAGTTCTGCA	197

FIG. 15B-3

CYP52A1A	613	TTACTTTTGAGGTCATAGGAGTTGCCGTGTGAGAGATCACAGAGATTATCACACTCACATTTATCGTAGTT	682
CYP52A2A	684	CTGCGCTTGAAACGGATTTCATGCACGAACGGAGA-TAAAAGATTACGT---AATTATCTCCTTGAGACA	749
CYP52A2B	506	CTGTAGTTGGAACGGATTTCATGCACGATCGGGAGA-TAACACG-----AGATTATCTCCTTAAGACA	565
CYP52A3A	636	C--CAATTTGACCTCGTTTCATGTGATAAAAGAAAAGCCAAAGGTAATT---AGCAGACGC---AATGGG	697
CYP52A3B	398	T--CAATTTATCCTCATTTCATGTGATAAAAGAGAGCCAAAGGTAATT---GGCAGACCCCCCAAGGGG	462
CYP52A5A	552	TTGATTTTG---TGTAAGGTTTGGATGTCAACCTACTCCGCACCTTCATGCA-GTGTGTGTGACACAAGG	617
CYP52A5B	626	TTGATTTTG---TGTAAGGTTTAGCACGTCACGCTACTCCGCACCTTTGT----GTGTAGGGAGCACACA---	685
		0	
CYP52A8A	1		567
CYP52A8B	502	GACACACTT---TCAACTGAGTTTGGTCTAGAAATTTTGCACATGCACGACA-AGGAAACTCTTACAAAG	266
CYP52D4A	198	GGTAAATTTGGATGTCAGGTAGTGGAGGGAGGTTTGTATCGGTTGTGTT-TTCTTCTTCCCTCTCTCTCTG	
CYP52A1A	683	TCCTATCTCATGCTGTGTGCTCTGTTGTTTCATGAGTTTGGATT--GTTGTACATTAAAGGAATCGCT	750
CYP52A2A	750	ATTTTAGCCGTGTTTCACACGCCCTTCTTTGTT-CTGAGCGAAGGAT--AAATAATTAGACTTCCACAGCT	816
CYP52A2B	566	ATTTTGGCCCTCATTCACACGCCCTTCTT-----CTGAGCTAAGGAT--AAATAATTAGACTTCCACAAAGTT	628
CYP52A3A	698	AACATGGAGTGGAAGCAATGGAAGCACGCC--AGGACGGAGTAATTTAGTCCACACTACATCTGGGGGT	766
CYP52A3B	463	AACACGGAGTAGAAAGCAATGGAACACACGCC--ATGACAGTGCCATTTAGCCCAACAACACATCTAGTATT	531
CYP52A5A	618	GTGTACTACGTGTGCGTGTGCGCCCAAGAGACA---GCCCAAGGGG--TGGTAGTGT-GTGTGTGGCGGAA	681
CYP52A5B	686	---TACTCCGTCTGCGCTGTGCGCCCAAGAGACG---GCCCAGGGG-----TAGTGT-GTGGTGGTGGAA	741
CYP52A8A	1	GAATTCCTTTGGATCTAATTCACGCTGATC---TTGCTAATCCT--TATCAACGTAAGTTGTGATCATT	62
CYP52A8B	568	--ACAACACTTGTGCTCTGATGCCACTTGATC---TTGCTAAGCCT--TATCAACGTAATTTGAGATCATT	630
CYP52D4A	267	ATTCAACCTCCACGTCCTCCTTCGGTTCTGTGTCTGTGAGTC--GTACTGTTGGATTAAAGTCCATC	334

FIG. 15C-I

CYP52A1A	751	GGAAAGCAAGCTAACTAAATTTTCTTTGTACAGGTACACTAACCTGTAAAACTTCACTGCCACGCCAG	820
CYP52A2A	817	CATTCTAAATTTCCGT---CACGGGAATATTGAA-----GGGGGTACATGTGGCCGCTGAA-	869
CYP52A2B	629	CATTAAATATCCGT---CACGGGAAACTGCAACAATAAGGAAGGGGGGTAGACGTAGCCGATGAA-	694
CYP52A3A	767	----TTTTTTTGTGGCAAGTACACACCTGGACT-TTAGTTTTTGCCTCCATAAAGTTAACAATCTAA-	830
CYP52A3B	532	CTTTTTTTTTTGTGCGCAGGTGCACACCTGGACT-TTAGTTATTGCCCCATAAAGTTAACAATCTCA-	599
CYP52A5A	682	GTGCATGTGACACA---ACGCGTGGTTCTGGCCAATGGTGGACTAAGTGCAGGTAAAGCAGCGACCTGAA	748
CYP52A5B	742	GTGCATGTGACACA---ATACCTGGTTCTGGCCAATGGGGATTTAGTGTAGGTAAAGCTGCCACCTGAA	808
CYP52A8A	63	GTTTGTCTGAATTAT--ACACACCAAGTGAAGAAATATGGTCTAATTTGCACGCTCCCACTGGCAATTGTG--	128
CYP52A8B	631	GTTTGTCTGAATTAT--ACACACCAAGTGAAGAAATCTGGTCTAATCTGCACGCTCATGGGCATTGTG--	696
CYP52D4A	335	GCATGTGTGAAAAAAGTAGCGCTTATTAGACAACCAAGTTTCGTTGGGGGGGTATCAGAAATAGTCTGTT	404
CYP52A1A	821	TCTTTCCTGATTGGGCAAGTGCACAAACTACA-ACCTGCAAAACAG---CACTCCGCTTGTACAGGTT	885
CYP52A2A	870	-TGTGGGG--CAGTAAACGCAGTCTCTC-----CTCTCCCAGGAATAGTGCAACGG	918
CYP52ACB	695	-TGTGGGGTCCAGTAAACGCAGTCTCTCTCCCCCCCCCCCCCCCCCTCAGGAATAGTACAACGG	763
CYP52A3A	831	-CCTTTGGC-TCTCCAACTCTCTCGCCCCCAAATAATTCGTTTTT-ACACCTCAAGCTAGCGACAGCAC	897
CYP52A3B	600	-CCTTTGGC-TCTCCAGTGTCTCCGCTCCAGATGCTCGTTTTT--ACACCTCGAGCTAACGACAACAC	665
CYP52A5A	749	ACATTCTCAACGCTTAAGACACTGGTGG-TAGAGATGCGGACCAGG-----CTATTCTTGTCTG-TGCTA	811
CYP52A5B	809	ACACTCCTCAACGCTTGAGACACTGGTGGGTAGAGATGCGGGCCAGGA--GGCTATTCTTGTCTG-TGCTA	875
CYP52A8A	129	-TGTTT-----GTGGGGGGGGGGGTGCACACATTTTGTAGTGCCA----TTCTTTGTGATTAC-CCCT	187
CYP52A8B	697	-TGTTT--GGGGGGGGGGGGGTGCACACATTTTGTAGTGCGAATGTTTGTGTTGCTGGTTCC-CCCT	762
CYP52D4A	405	GTGCACGACCATGAGTATGCAACTTGACGAGACGTCGTTAGGA-----ATCCACAGAATGATAGCAGGAA	469

FIG. 15C-2

CYP52A1A	886	GTCTCCTCTCAACCAACAAAAAATAAGATTAAACTTTCTTTGCTCATGCATCAATCGGAGTTATCTCTG	955
CYP52A2A	919	AGGAAGGATAACGGATAGAAAGCGGAATGCGAGGAAAAT - TTTGAACGCGCAAGAAAAGCAATATCCGG	986
CYP52A2B	764	GGGAAGGATAACGGATAGCAAGTGGAATGCGAGGAAAAT - TTTGAATGCGCAAGGAAAGCAATATCCGG	831
CYP52A3A	898	AACACCCATTAGAGGAATGGGCAAAAGTTAAACACTTTTGGCTTCAATGATTCTTATTCGCTACTACATT	967
CYP52A3B	666	AACACCCATGAGGGGAATGGG - CAAAGTTAAACACTTTTGGTTTCAATGATTCTTATTCGCTACT - - - -	729
CYP52A5A	812	CCCGCGCATGGA - AAATCAACTGCGGGAAGAA - TAAATTTATCCGTAGAAATCCACAGAGCG - - - - - G	872
CYP52A5B	876	CCCG - TGCACGGA - AAATCGATTGAGGGAAGAA - CAAATTTATCCGTGAAATCCACAGAGCG - - - - - G	935
CYP52A8A	188	CCCCCTATCAT - - - TCATTTCCACAGGATTAG - TTTTTCCTCACTGGAATTCGCTGTCC - - - - -	244
CYP52A8B	763	CCCCCTCCCCCTATCATGCCCCACAGGATTAG - TTTTTCCTCACTGGAATTCGCTGTCC - - - - -	822
CYP52D4A	470	GCTTACTACGTGAGAGATTCTGCTTAGAGGATG - TTCTCTTCTTGTGATTCCATTAGGTGGGTATCAT	537

FIG. 15C-3

CYP52A1A	956	A--AAGAGTTGCCCTTTGTGTAATGTGTGTCCTCCAAA--CTCAAACTGCAGAACTAACCACAGAAATGAT-----	1016
CYP52A2A	987	GCTACCAGGTTTTGAGCCAGGGAACACACTCCTATTTCTGTCTCAATGACTGAACATAGAAAAA-----	1050
CYP52A2B	832	GCTATCAGGTTTTGAGCCAGGGAACACACTCCT--CTTCTGCACAAAAA--CTTAACGTAGACAAAAA-----	900
CYP52A3A	968	CTTCTCTTGTGTTTTGTGCTTTGAATTGCACCATGTGAAATAAACGACAAATTATATATACCTTTTCAATC----	1034
CYP52A3B	730	---CTCTTGTGTTTTGTGTTTTGTGATTTTGACCAATGTGAAATAAACGACAAATTATATATACCTTTTCGTC---	793
CYP52A5A	873	A--TAAATTTGCCACCTCCATCATCAACACAG--CCGCCACTAACTACATCACTCCCTATTTT-----	933
CYP52A5B	936	A--TAAATTTGTCACATTGCTGCGTTGCCAC-----CCACAGCATTTCTC-----	978
CYP52A8A	245	-----ACCTGTCAACCCCCCCCCCCCCCCCC--CCACTGCC--CTACCCCTGCCCTGC-----	293
CYP52A8B	823	-----ACCTGTCAACCCCCCTCAC-----TGCCCTGCCCTGC-----	853
CYP52D4A	538	CTCCGGTGGTGACAACTTGACACAAAGCAGTTCCGAGAACCCACCAACAATCACCATTCCAG-----	601
*			
CYP52A1A	1017	TTCCCTCACAATTATATAAACTCACCACACATTTCCACAGACCGTAATTTTCATGTCTCAC-TTCTCTTTT	1085
CYP52A2A	1051	-----CACCAAGACGCAATGAAACGCACATGGACATTTAGACCTCCCCACATGTGATAGTTTGTCTTAAC	1115
CYP52A2B	901	AACTCCACCAAGACACAAATGAATCGCACATGGACATTTAGACCTCCCCACATGTGAAAGCTTCTCTGGCG	970
CYP52A3A	1035	CCTCCTCCTATATCTCTTTTTTGCTAC-ATTTGTTTTTTTACGTTTTCTTGCTTTTGCACTCTCCCACTCCC	1103
CYP52A3B	794	TGTCCTCCAATGTCTCTTTTTTGCTGCCATTTTGCTTTTTTGCTTTTGGCACTCTCTCCCACTCCC	863
CYP52A5A	934	CTCTCTCTCTTTTGTCTTACTCCGCTCCCGTTTCTCTTAGCCACAGATACACCCCACT-GCAAAACAGCA	1002
CYP52A5B	979	TTTTCTCTCTCTTTGTCTTACTCCGCTCCTGTTTCTCTTATCCAGAAATACACACAACTCATATAAAGAT	1048
CYP52A8A	294	CCTGCACGTCCTGTGTTTTGTGTGTGTCTTTTCCACGCTATAAAGCCCTGGCGTCCGGCCAAAGGTTTT	363
CYP52A8B	854	CCTGCACGCCCTGTGTTTTGTGTGTGGCACTCCCAAGCTATAAAGCCCTGGCGTACGGCCAAAGTTTT	923
CYP52D4A	602	TATCACTTCTACATGTCAACCTACGATGATCTCATCACCATCTAGTTTCTTTGGCAATCGTTTATTTGTT	671

FIG. 15D-I

CYP52A1A	1086	GCTCTCTTTTACTTAGTCAGGTTTGATAACTTCCTTTTATTATACCCTAATCTTATTATTATTATTATTC	1155
CYP52A2A	1116	AGA-----AAAGTATAATAAGAACCCATGCCGTCCCTTTCTTTGCGCGCTTCAACTTTTTTTTTTTA	1179
CYP52A2B	971	AAAGCAAAAAAAGTATAATAAGGACCCATGCCCTTCCCTCTTCCTGGGCGGTTTCAACTTTTTTCTTTTCT	1040
CYP52A3A	1104	ACAA-----AGAAAAAATACTACACTAAGTCGCTCTTCTCCATCGTTT	1146
CYP52A3B	864	ACAATCAGTCAGCAACACACAAAGAAATAAAAAACCTACACTATGTCGCTCTTCTCCATCGTTT	933
CYP52A5A	1003	GCA--ACAATTATAAAGATACGCC-----AGGCCACCTTCTTTTCTTCACTTTTGTGACTGC-A	1064
CYP52A5B	1049	ACG--CTAGCCCAGCTGCTTTCT-----TTTCTTCACTTTTGGTGCTGCTTTTGGCTGC-T	1110
CYP52A8A	364	TCCACCCAGCCAAAAACAGCTCTAAAAAATTTGGTTGATCCCTTTTGGTTGCAAGGTTT---CCAC-C	429
CYP52A8B	924	TCCTCACAGCCAAAAAA-----AATTGGCTGATCCTTTTGGGCTGCAAGGTTTTCACCCAC-C	982
CYP52D4A	672	ATGGGTCAACATCCAATACAACCTCCACCA--TGAAGAAGAAAAACGGAAAGCAGAATACCAGAATGACA	739
			*
CYP52A1A	1156	ATTTATACCAACCAACC--AACCATGGCCACACAAGAAATCATCGATTCTGTACTTCCGTACTTGACCAA	1223
CYP52A2A	1180	TCCTT-----ACACACATCAGACCA-TGACTGTACACGATATTATCGCCACATACATTCAACCAA	1236
CYP52A2B	1041	TTGTCATCAACACACACACACCTCAGACCA-TGACTGCACAGGATATTATCGCCACATACATCACC	1109
CYP52A3A	1147	GCCC-----AAGAGGTTCTCGCTACCACTAGTCCTTACATCGAGTACTTTCTTGACA-ACTACACCAG	1208
CYP52A3B	934	GCTC-----AGGAGGTTCTCGCTACCACTAGTCCTTACATCGAGTACTTTCTTGACA-ACTACACCAG	995
CYP52A5A	1065	ACTTCTACAATCCACACAGCCACCAAGCCGCTATGATTGAACAACTCCTAGAATAT-----	1127
CYP52A5B	1111	ACTTCTACAACC-----ACCACCACCAACCACCATGATTGAACAAATCCTAGAATAT-----	1166
CYP52A8A	430	ACCACCTCCACCA--CCTCAACTATTGAAACAA--AAGATGCTCGATCAGATCTTACATTACT-----	488
CYP52A8B	983	ACCACCACCA--CCTCAACTATTGAAACAA--AGGATGCTCGACCAAGATCTTCCATTACT-----	1041
CYP52D4A	740	GTGTG----AGTTCCTGACCATTGCTAATCTA-TGGCTATATCTAGTTTGGTATCGTGGGATG-----	797
			*

FIG. 15D-2

CYP52A1A	1224	ATGGTACACTGTGATTACTGCAGCAGTATTAGTCTTCCTTATCTCCACAAACATCAAGAAC	1293
CYP52A2A	1237	ATGGTACGTGATAGTACCACCTCGCTTTGATTGCTTATAGAGTCTCGACTACTTCTATGGCAGATACTTG	1306
CYP52A2B	1110	ATGGTACGTGATAGTACCACCTCGCTTTGATTGCTTATAGGGTCCCTCGACTACTTTTACGGCAGATACTTG	1179
CYP52A3A	1209	ATGGTACTACTTTCATACCTTTGGTGCCTTCTTTGAACTTTATAAGTTTGCTCCACACAAGGTACTTG	1278
CYP52A3B	996	ATGGTACTACTTTCATACCTTTGGTGCCTTCTTTGAACTTTGAACTTTCATCAGCTTGCTCCACACAAAAGTACTTG	1065
CYP52A5A	1128	--GGTATGTCGTTGTGCCAGTGTGTACATCATCAAACTCCTTGCATACACAAAGACTCGCGTCTTG	1195
CYP52A5B	1167	--GGTATGTCGTTGTGCCAGTGTGTACATCATCAAACTCCTTGCATACACAAAGACTCGCGTCTTG	1234
CYP52A8A	489	--GGTACATTGTCTTGCCATTGTTGGCCATTATCAACCAAGATCGTGGCTCATGTCAGGACCAATTATTG	556
CYP52A8B	1042	--GGTACATTGTCTTGCCATTGTTGGTCATTATCAAGCAGATCGTGGCTCATGTCAGGACCAATTATTG	1109
CYP52D4A	798	-TGATCTGTGTCGTCCTTCAATTTGCGTTTGTGTTTATTTCGGGTAT-GAATATTGTTATACTAAATACTTG	865

FIG. 15D-3

CYP52A1A	1294	GCAAGAAATTGAAATGTGTGATCCACCATACTTGAAGGATGCCCGTCTCACTGGTATTCTGTCTTTGA	1363
CYP52A2A	1307	ATGTACAAGCTTGGTGCTAAACCATTTTCCAGAAACAGACAGCGGTGTTTCGGATTCAAGCTCCGC	1376
CYP52A2B	1180	ATGTACAAGCTTGGTGCTAAACCGTTTTCAGAAACAAACAGACGGTTATTTCCGGATTCAAGCTCCAC	1249
CYP52A3A	1279	GAACGAGGTTCCACGCCAAGCCACTCGGTAACTTTGTCAAGGACCCCTACGTTTGGTATCGCTACTCCGT	1348
CYP52A3B	1066	GAACGAGGTTCCACGCCAAGCCGCTCGGTAACTCGTGTGGATCCTACGTTTGGTATCGCTACTCCGT	1135
CYP52A5A	1196	ATGAAAAGTTGGTGCTGCTCCAGTCACAAACAAAGTTGTACGACAACGTTTCCGGTATCGTCAATGGAT	1265
CYP52A5B	1235	ATGAAACAGTTGGGTGCTGCTCCAATCACAAACAGTTGTACGACAACGTTTTCGGTATCGTCAACGGAT	1304
CYP52A8A	557	ATGAAGAAATTGGGTGCTAAGCCATTCAACACGTCACGTCGCGGTGGTTGGCTTCAAATTCGGCC	626
CYP52A8B	1110	ATGAAGAAATTGGGCGCTAAGCCATTCAACACATGTCCAACCTAGACGGGTGGTTGGCTTCAAATTCGGCC	1179
CYP52D4A	866	ATGCACAAACATGGCGCTCGAGAAATCGAGAAATGTGATCAACGATGGGTCTTGTGGTTCCGCTTACCTT	935

* * *

CYP52A1A	1364	TCGCCGCATCAAGGCCAAGAACGACGGTAG-ATTGGCTAAGTTTGCC-----GATGAAGTTT	1421
CYP52A2A	1377	TTGAATTGTTGAAGAAAGAGAGCGGCTAC-CCTCATAGACTTCACA-----CTCAGCGTATC---C	1436
CYP52A2B	1250	TTGAATTGTTAAAGAAAGAGAGTGACGGTAC-CCTCATAGACTTCACT-----CTCAGCGTATC---C	1309
CYP52A3A	1349	TGCTTTTGATCTACTTGAAGTCGAAAGGTAC-GGTCAATGAAGTTTGCTTGGGCGCTCTGGAAACAACAAGT	1417
CYP52A3B	1136	TGATCTTGATCTACTTAAAGTCGAAAGGTAC-AGTCATGAAGTTTGCCTGGAGCTTCTGGAAACAACAAGT	1204
CYP52A5A	1266	GGAAGGCTCTCCAGTTCAAGAAAGAGGGCAGGGCTCAAGAGTACAACG-----ATTACAAGTTTG---	1325
CYP52A5B	1305	GGAAGGCTCTCCAGTTCAAGAAAGAGGGCAGAGCTCAAGAGTACAACG-----ATCACAAGTTTG---	1364
CYP52A8A	627	GTGAATTCTCAAGCAAAAAGTGCTGGGAG-CTGGTTGATTAAATC-----ATCTCCCGTTT-----	684
CYP52A8B	1180	GTGAATTCTCAAGCTAAAAGTGCTGGGAG-GCAGGTTGATTAAATC-----ATCTCCCGTTT-----	1237
CYP52D4A	936	TGCTACTCATCGAGGCCAGCAATGAGGCGG-ACCTATCGAGTTCAGT-----GTCAAGAGATTCGAGT	998

* * *

FIG. 15E-1

CYP52A1A	1422	----	CGACGAGTACCCAAACACACCTTCTACTTGTCTGTGTTGCCGGTGTCTTTGAAGATTGTGATGACTGT	1487
CYP52A2A	1437	ACGATCTCGATCGTCCCGATATCCCAACTTTTCACATTCCCGGTCTTTTCCATCAACCTTGTCAATACCCCT	1506	
CYP52A2B	1310	AAGCGTCAATCGTCCAGATATCCAACTTTTACATTTCCCAATCTTTTCCATCAACCTTATCAGCACCCCT	1379	
CYP52A3A	1418	ACATCGTCAGAGACCCAAAGTACAAAGACAACTGGGCTCAGGATTGTTGGCCTCCCATTTGATTGAAACCAT	1487	
CYP52A3B	1205	ACATTGTCAAAGACCCAAAGTACAAAGACCACTGGCCTTAGAATTGTGCGCCTCCCATTTGATTGAAACCAT	1274	
CYP52A5A	1326	ACCACTCCAAGAACCCCAAGCGTGGGCACCTACGTGAGTATTTCTTTTCGGCACCCAGGATCGTGTGACCAA	1395	
CYP52A5B	1365	ACAGCTCCAAGAACCCCAAGCGTGGGCACCTATGTGAGTATTTCTTTTGGCACCAAGATTGTCGTGACCAA	1434	
CYP52A8A	685	-----CCACGA----	TAATGAGGACACTTCTTCAGCTATGCTTTTGGCAACCATGTGGTGTTCACCCAG	744
CYP52A8B	1238	-----CCACGA----	TAATGAGGACACTTCTTCAGCTATGCTTTTGGCAACCATGTGGTGTTCACCCAG	1297
CYP52D4A	999	-CGGCGCCACAT--CCACAGAACAGACATTTGGTCAACCGGGCATTGAGCGTTCTGTGATACTCACCAA	1065	
		*	* * *	
CYP52A1A	1488	TGACCCAGAAAAACATCAAGGCTGTCTTTGGCCACCCAAATTCACCTGACTTCTCTTGGGTACCAGACACGCC	1557	
CYP52A2A	1507	TGAGCCGGAGAACATCAAGGCCATCTTTGGCCACTCAGTTCAACGATTTCTCTCTTGGGTACCAGACACTCG	1576	
CYP52A2B	1380	TGAGCCGGAGAACATCAAGGCTATCTTTGGCCACCCAGTTCAACGATTTCTCTCTTGGGTACCAGACACTCG	1449	
CYP52A3A	1488	GGACCCAGAGAACATCAAGGCTGTTTGGCTACTCAGTTCAATGATTTCTCTTTGGGAACCCAGACACGAT	1557	
CYP52A3B	1275	AGACCCAGAGAACATCAAAAGCTGTGTGGCTACTCAGTTCAACGATTTCTCTCTTGGGAACCTAGACACGAT	1344	
CYP52A5A	1396	AGATCCAGAGAAATATCAAAAGCTATTTTGGCAACCCAGTTTGGTGATTTTCTTTTGGGCAAGAGGCACACT	1465	
CYP52A5B	1435	GGATCCAGAGAAATATCAAAAGCTATTTTGGCAACCCAGTTTGGCGATTTTCTTTTGGGCAAGAGACACGCT	1504	
CYP52A8A	745	GGACCCCGAGAAATATCAAGGCGCTTTTGGCAACCCAGTTTGGTGATTTTTCATTTGGGCAAGAGGTCAGG	814	
CYP52A8B	1298	GGACCCCGAGAAATATCAAGGCGCTTTTGGCAACCCAGTTTGGTGATTTTTCATTTGGGAAGCAGGGTCAAA	1367	
CYP52D4A	1066	GGACCCAGTGAATATCAAAAGCGATGCTATCGACCCAGTTTGTGATGACTTTTCCCTTGGGTTGAGACTACAC	1135	
		** ** *	** ** *	**

FIG. 15E-2

[illegible]

FIG. 15E-3

CYP52A1A	1628	TGTTGAGACCA	CAGTTTGCTAGAGACCAGATTGGACACAGTTAAAGCCTTGGAA	CCACACATCCAAATCAT	1697
CYP52A2A	1647	TGTTGAGACCA	CAGTTTGCCAGAGAACAGATTTCACAGTCAAGTTGTTGGAGCCA	CACAGTTTACGGTGT	1716
CYP52A2B	1520	TGTTGAGACCA	CAGTTTGCCAGAGAACAGATTTCACAGTCAAGTTGTTGGAGCCA	CACATGCAGGTGT	1589
CYP52A3A	1628	TGTTGAGACCA	CAGTTTGCTAGAGAACAGTTTCTCAGTCAAGTTGTTGGAGCCA	CACAGTTTACGGTGT	1697
CYP52A3B	1415	TGTTGAGACCA	CAGTTTGCTAGAGAACAGTTTCCACGTCAAGTTGTTGGAA	CCACACAGTTTACGGTGT	1484
CYP52A5A	1536	TGTTGAGACCA	CAGTTTGCCAGAGAACAAAGTTGCTCATGTGACGTCGTTGGA	ACCACACTTCCAGTTGT	1605
CYP52A5B	1575	TGTTGAGACCA	CAGTTTGCCAGAGAACAAAGTTGCTCATGTGACGTCGTTGGA	ACCACACTTCCAGTTGT	1644
CYP52A8A	885	TGTTGAGACCA	CAGTTTGCCAGAGAACAAAGTTGCTCATGTGACGTCGTTGGA	ACCACACTTCCAGTTGT	954
CYP52A8B	1438	TGTTGAGACCA	CAGTTTGCCAGAGAACAAAGTTGCTCATGTGACGTCGTTGGA	ACCACACTTCCAGTTGT	1507
CYP52D4A	1206	TGTTGCGTCCG	CAATTTGCCAAAGATCGGGTTTCTCATATCCTGGATCTAGA	ACCGCATTTTGTGTGCT	1275
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CYP52A1A	1698	GGCTAAGCAGAT	CAAGTTGAACCAAGGAAAGACTTTCGATATCCAAGAA	TTGTTCTTTAGATTACCGTC	1767
CYP52A2A	1717	CTTCAAAACAC	GTGAGAAAGGCACAGGGCAAGACTTTTGACATCCAGGAA	TTGTTTTCAGATTGACCGTC	1786
CYP52A2B	1590	CTTCAAGCAC	GTGAGAAAGGCACAGGGCAAGACTTTTGACATCCCAAGAA	TTGTTTTCAGATTGACCGTC	1659
CYP52A3A	1698	CTTCAAGCAC	GTGAGAAAGGCACAGGGCAAGACTTTTGACATCCCAAGAA	TTGTTTTCAGATTGACCGTC	1767
CYP52A3B	1485	CTTCAAGCAC	GTGAGAAAGGCACAGGGCAAGACTTTTGACATCCCAAGAA	TTGTTTTCAGATTGACCGTC	1554
CYP52A5A	1606	GAAGAAAGCAT	ATTCTTAAAGCACAAAGGGTGAATACTTTGATATCCAGGAA	TTGTTTTCAGATTTACCGTT	1675
CYP52A5B	1645	GAAGAAAGCAT	ATTCTTAAAGCACAAAGGGTGAATACTTTGATATCCAGGAA	TTGTTTTCAGATTTACCGTT	1714
CYP52A8A	955	GAAGAAAGCAT	ATTCTTAAAGCACAAAGGGTGAATACTTTGATATCCAGGAA	TTGTTTTCAGATTTACCGTT	1024
CYP52A8B	1508	GAAGAAAGCAT	ATTCTTAAAGCACAAAGGGTGAATACTTTGATATCCAGGAA	TTGTTTTCAGATTTACCGTT	1577
CYP52D4A	1276	TCGGAAGCACAT	TGATGGCCACAATGGAGACTACTTCGACATCCAGGAGCTCTACT	TCCGGTTCTCGATG	1345
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FIG. 15F-1

CYP52A1A	1768	GACACCGCTACTGAGTCTCTGTTTGGTGAATCCGTTTCACTCCTTGACGATGAAAAATTGGGCATCCCAA	1837
CYP52A2A	1787	GACTCCGCCACCGAGTTTCTGTTTGGTGAATCCGTTGAGTCCCTTGAGAGATGAATCTATCGGCATGTCCA	1856
CYP52A2B	1660	GACTCCGCCACCTGAGTTTCTGTTTGGTGAATCCGTTGAGTCCCTTGAGAGATGAATCTATTTGGGATGTCCA	1729
CYP52A3A	1768	GACTCCGCCACCGAGTTCTGTTTGGTGAATCCCTGCTGAATCCCTTGAGGGACGAAATCTATTTGGATTGACCC	1837
CYP52A3B	1555	GACTCCGCCACCGAGTTCTGTTTGGTGAATCCCTGCTGAATCCCTTGAGAGACGACTCTGTTGGTTTGACCC	1624
CYP52A5A	1676	GATTCCGCCACCGAGTTCTTATTTGGTGAGTCCGTCGACTCCTTAAAGGACGAAATCTATTTGGTATCAACC	1745
CYP52A5B	1715	GACTCCGCCACCGAGTTCTTATTTGGTGAGTCCGTCGACTCCTTAAAGGACGAAATCTATTTGGTATCAACC	1784
CYP52A8A	1025	GACTCCGCCACCGAGTTCTTATTTGGTGAGTCCGTCGACTCCTTAAAGGACGAGGAAATTTGGCTACGACA	1094
CYP52A8B	1578	GATTCCGCCACCGAGTTCTTATTTGGTGAGTCCGTCGACTCCTTAAAGGACGAGGAAATTTGGCTACGATA	1647
CYP52D4A	1346	GATGTGGCGACGGGGTTTTGTTTGGCGAGTCTGTGGGGTCTGTTGAAAGACGAAAGATCGGAGG-----	1408
		** ** * * * * * * * * * * * * * *	
CYP52A1A	1838	CTCCAAACGAAA---TCCCAGGAAGAGAAAACTTTGCCGCTGCTTTCAACGTTTCCCAACACTACTTGGC	1904
CYP52A2A	1857	TCAATGCGCTTGACTTTGACGGCAAGCTGGCTTTGCTGATGCTTTTAACTATTTCGCAGAAATTAATTGGC	1926
CYP52A2B	1730	TCAATGCACCTTGACTTTGACGGCAAGCTGGCTTTGCTGATGCTTTTAACTACTCGCAGAACTATTGGC	1799
CYP52A3A	1838	CAACCAACCAAGGATTTGATGGCAGAGAGATTTGCTGACGCTTTCAACTATTTCGCAGACTTACCAGGC	1907
CYP52A3B	1625	CAACCAACCAAGGATTTGATGGCAGAGAGATTTGCTGACGCTTTCAACTACTTCGCAGACTTACCAGGC	1694
CYP52A5A	1746	AAGACGATATAGATTTTCTGCTGGTAGAAAGGACTTTGCTGAGTCGTTCAACAAAGCCCCAGGAATACTTGGC	1315
CYP52A5B	1785	AAGACGATATAGATTTTCTGCTGGTAGAAAGGACTTTGCTGAGTCGTTCAACAAAGCCCCAGGAATACTTGGC	1854
CYP52A8A	1095	CGAAAGACATGT---CTGAAGAAAGACCGCAGATTTGCCGACGCGTTCAACAAAGTCGCAAGTCTACGTGGC	1161
CYP52A8B	1648	CGAAGGACATGG---CTGAAGAAAGACCGCAAAATTTGCCGACGCGTTCAACAAAGTCGCAAGTCTATTGTC	1714
CYP52D4A	1409	-----TTCCTGGAAGCATTCATAGTCGCAGAAAGTATTGGC	1445
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FIG. 15F-2

CYP52A1A	1905	CACCAGAGTTACTCCAGACTTTTACTTTTTGACCAACCTTAAGGAATTCAGAGACTGTAAACGCCAAG	1974
CYP52A2A	1927	TTCGAGAGCGGTTATGCAACAATGTACTGGGTGTGAACGGGAAAAAGTTTAAAGGAGTGCAACGCTAAA	1996
CYP52A2B	1800	TTTCGAGAGCGGTTATGCAACAATGTACTGGGTGTGAACGGGAAAAAGTTTAAAGGAGTGCAACGCTAAA	1869
CYP52A3A	1908	CTACAGATTTTGTGCAACAATGTACTGGATCTTGAATGGCTCGGAATTCAGAAAGTCGATTGCTGTC	1977
CYP52A3B	1695	CTACAGATTTTGTGCAACAATGTACTGGATTTTGAATGGCGCGGAATTCAGAAAGTCGATTGCCATC	1964
CYP52A5A	1816	TATTAGAACCTTGGTGCAGACGTTCTACTGGTTGGTCAACAACAAGGAGTTTAGAGACTGTACCAAGCTG	1885
CYP52A5B	1855	TATTAGAAATTTGGTGCAGACCTTCTACTGGTTGATCAACAACAAGGAGTTTAGAGACTGTACCAAGCTG	1924
CYP52A8A	1162	CACCAGAGTTGCTTTACAGAACTTGTAAGTTGGTCAACAACAAGAGTTCAAGGAGTGCAATGACATT	1231
CYP52A8B	1715	CACCAGAGTTGCTTTACAGACATTTGTAAGTTGGTCAACAACAAGAGTTCAAGGAGTGCAACGACATT	1784
CYP52D4A	1447	AACTAGGGCAACGTTGCACGAGTTGTACTTTCTTTGTGACGGGTTTAGGTTTCGCCAGTACAAACAAGGTT	1516

FIG. 15F-3

CYP52A1A	1975	GTCCACCACTTGGCCCAAGTACTTTGTCAACAAGCCCTTGAACTTTACTCTGAAGAACTCGAAGAGAAAT	2044
CYP52A2A	1997	GTGCACAAAGTTTGTGCTGACTACTACGTCAACAAGGCTTTGGACTTTGACGCTGAACAAATTGGAAAAGGAGG	2066
CYP52A2B	1870	GTGCACAAAGTTTGTGCTGACTATTACGTGACCAAGGCTTTGGACTTTGACACCTGAACAAATTGGAAAAGCAGG	1939
CYP52A3A	1978	GTGCACAAAGTTTGTGCTGACCACTATGTGCAAAAAGGCTTTGGAGTTGACCGACGATGACTTGCAGAAAACAAG	2047
CYP52A3B	1765	GTGCACAAAGTTTGTGCTGACCACTATGTGCAAAAAGGCTTTGGAGTTGACCGACGATGACTTGCAGAAAACAAG	1834
CYP52A5A	1886	GTGCACAAAGTTTACCAACTACTATATGTTTCAAGAAAGCTTTGGATGCTAGCCCAAGAGAGCTTGAAAAGCAAA	1955
CYP52A5B	1925	GTGCACAAAGTTTACCAACTACTATGTTTCAAGAAAGCTTTGGATGCTAGCCCAAGAGAGCTTGAAAAGCAAG	1994
CYP52A8A	1232	GTCCACAAAGTTTACCAACTACTATGTTTCAAGAAAGCTTTGGATGCTAGCCCAAGAGAGCTTGAAAAGCAAG	1301
CYP52A8B	1785	GTCCACAAAGTTTACCAACTACTATGTTTCAAGAAAGCTTTGGATGCTAGCCCAAGAGAGCTTGAAAAGCAAG	1854
CYP52D4A	1517	GTCCGAAAGTTCTGCAGCCAGTGTGTCCACAAGGCTTAGATGTTTGACCCGGAAGACACC-----A	1577
		** * * * * * * * * * * * * * * *	
CYP52A1A	2045	CCAAAGTCCGGTTACGTTTCTTGTACGAATTGGTTAAGCAAAACCAGAGATCCAAAAGGCTTGAAGATCA	2114
CYP52A2A	2067	ATGGTT-----ATGTGTTTTTGTACGAATTGGTCAAGCAAAACCAGAGACAAGCAAGTGTGTGAGAGACCA	2130
CYP52A2B	1940	ATGGTT-----ATGTGTTCTTGTACGAGTTGGTCAAGCAAAACCAGAGACAGGCAAGTGTGTGAGAGACCA	2003
CYP52A3A	2048	ACGGCT-----ATGTGTTCTTGTACGAGTTGGCTAAGCAAAACCAGAGACCCCAAGGCTTGTGAGAGACCA	2111
CYP52A3B	1835	ACGGCT-----ATGTGTTCTTGTACGAGTTGGCTAAGCAAAACCAGAGACCCCAAGGCTTGTGAGAGACCA	1898
CYP52A5A	1956	GTGGGT-----ATGTGTTCTTGTACGAGCTTGTCAAGCAGACAAGAGACCCCAATGTGTTCGCTGACCA	2019
CYP52A5B	1995	GCGGGT-----ATGTGTTCTTGTATGAGCTTGTCAAGCAGACGAGAGACCCCAAGGCTTGTGCTGACCA	2058
CYP52A8A	1302	GCGGGT-----ATGTGTTCTTGTATGAGCTTGTCAAGCAGACGAGAGACCCCAAGGCTTGTGCTGACCA	1365
CYP52A8B	1855	GCGGGT-----ATGTGTTCTTGTACGAGCTTGTCCAAAGCAGACGAAAAGACCCCAATGTGTTCGCTGACCA	1918
CYP52D4A	1578	GCGAGT-----ACGTGTTTCTCCGGAGTTGGTCAACACACTCGAGATCCCGTTGTTTACAAAGACCA	1641
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FIG. 15G-I

CYP52A1A	2115	ATTGTTGAACATTATGTTGCCGGAAGAGACACCACTGCCGGTTTGTGTCTCTTTCCTTTGCTTTGTTGAATTG	2184
CYP52A2A	2131	ATTGTTGAACATCATGTTGCTGTTAGAGACACCAACCCCGCGTTTGTGTGCTGTTTCTTTTGAATTG	2200
CYP52A2B	2004	GTTGTTGAACATCATGTTGCCGGTAGAGACACCAACCCCGCGTTTGTGTGCTGTTTCTTTTGAATTG	2073
CYP52A3A	2112	GTTATTGAACATTTTGTGTTGCCGGTAGAGACACCAACCCCGCGTTTGTGTGCTGTTTCTTACGAGTTG	2181
CYP52A3B	1899	GTTGTTGAACATTTTGTGTTGCCGGTAGAGACACCAACCCCGCGTTTGTGTGCTGTTTCTTACGAGTTG	1968
CYP52A5A	2020	GTCATTGAACATCTTGTGTTGCCGGTAGAGACACCACTGCTGGGTTGTGTGCTGTTGCTGTTGAGTTG	2089
CYP52A2B	2059	GTCATTGAACATCTTGTGTCAGGAAGAGACACCACTGCTGGGTTGTGTGCTGTTGCTGTTGAGTTG	2128
CYP52A8A	1366	GTCATTGAACATCTTGTGTCAGGAAGAGACACCACTGCTGGGTTGTGTGCTGTTGCTGTTGAGTTG	1435
CYP52A8B	1919	GTCATTGAACATCTTGTGTCAGGAAGAGACACCACTGCTGGGTTGTGTGCTGTTGCTGTTGAGTTG	1998
CYP52D4A	1642	AGCGTTGAACGTCCTTGTGTCAGGACGAGACACCAACCCCGTCGTTATTATCGTTTGCAACATTTGAGCTA	1711
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CYP52A1A	2185	GCTAGACACCCAGAGATGTGGTCCAAGTTGAGAGAAGAAATCGAAGTTAACTTTGGTGTGGTGAAGACT	2254
CYP52A2A	2201	GCCAGAAA CCCAGAA GTTACCAACAAGTTGAGAGAAGAAATGAGGACAAAGTTTGGACTCGGTGAGAAATG	2270
CYP52A2B	2074	GCCAGAAA CCCAGAGGTGACCAACAAGTTGAGAGAAGAAATCGAGGACAAAGTTTGGTCTTTGGTGAGAAATG	2143
CYP52A3A	2182	TCAAGAAA CCCCTGAGGTGTTTGCTAAGTTGAGAGAGGAGTGGAACAAACAGATTGGACTCGGTGAAGAAG	2251
CYP52A3B	1969	TCGAGAAA CCCCTGAAGTGTGTCCTAAGTTGAGAGAGGAGTGGAACAAACAGATTGGACTCGGCGAAGAGG	2038
CYP52A5A	2090	GCCAGACACCCAGAGATCTGGGCCAAGTTGAGAGAGGAAATGAAACAAACAGTTTGGTCTTTGGAGAAAGACT	2159
CYP52A5B	2129	GCCAGAAA CCCACACATCTGGGCCAAGTTGAGAGAGGAAATGAAACAGCAGTTTGGTCTTTGGAGAAAGACT	2198
CYP52A8A	1436	GCCAGAAA CCCACACATCTGGGCCAAGTTGAGAGAGGAAATGAAACAGCAGTTTGGTCTTTGGAGAAAGACT	1505
CYP52A8B	1989	GCCAGGAA CCCACACATCTGGGCCAAGTTGAGAGAGGAAATGAAATCAGCTTTGGCTGGGTGAGGACT	2058
CYP52D4A	1712	GCCCAGGAATGACCACATGTGGAGGAAGCTACGAGAGGAGTT-----ATCCTGA---CGATGGGACCG	1771
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FIG. 15G-2

CYP52A1A	2255	CCCCGCTTGAAGAAATTACCTTCGAAGCCCTTGAAGAGATGTGAATACTTGAAGGCTATCCTTAACGAAAC	2324
CYP52A2A	2271	CTAGTGTGTAAGACATTTCCCTTTGAGTCGTTGAAGTCCTGTGAATACTTGAAGGCTGTTCTCAACGAAAC	2340
CYP52A2B	2144	CTCGTGTGTAAGACATTTCCCTTTGAGTCGTTGAAGTCATGTGAATACTTGAAGGCTGTTCTCAACGAAAC	2213
CYP52A3A	2252	CTCGTGTGTAAGAGATCTCGTTTGAGTCCTTTGAAGTCTTGTGAGTACTTGAAGGCTGTCAATGAATGAAC	2321
CYP52A3B	2039	CTCGTGTGTAAGAGATCTCTTTTGAGTCCTTTGAAGTCTTGTGAGTACTTGAAGGCTGTCAATGAAGC	2108
CYP52A5A	2160	CTCGTGTGTAAGAGATTACCTTTGAGAGCTTTGAAGAGATGTGAGTACTTGAAGGCTTCCCTTAATGAAC	2229
CYP52A5B	2199	CTCGTGTGTAAGAGATTACCTTTGAGAGCTTTGAAGAGATGTGAGTACTTGAAGGCTTCCCTTAACGAAAC	2268
CYP52A8A	1506	CTCGTGTGTAAGAGATTACCTTTGAGAGCTTTGAAGAGATGTGAGTACTTGAAGGCTGTTGAACGAAAC	1575
CYP52A8B	2059	CTCGTGTGTAAGAGATTACCTTTGAGAGCTTTGAAGAGATGTGAGTACTTGAAGGCTGTTGAACGAAAC	2128
CYP52D4A	1772	TCCAG--TGATGAAATAACCGTGGCCGGTTGAAGAGTTGCCGTTACCTCAAAGCAATCCTAAACGAAAC	1839

FIG. 15G-3

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FIG. 15H-2

CYP52A1A	2605	GCCTTGACTGAAGCTTCTTATGTGATCACTAGATTGGCCCCAGATGTTTGAAACTGTCTCATCTGATCCAG	2674
CYP52A2A	2621	GCCTTGACAGAAAGCTTCGTATGTCACTGTCAAGTTGCTCCAGGAGTTTGCACACTTGTCTATGGACCCAG	2690
CYP52A2B	2494	GCCTTGACAGAAAGCTTCGTATGTCACTGTCAAGTTGCTCCAGGAGTTTGGACACTTGTCTATGGACCCCA	2563
CYP52A3A	2602	GCCTTGACCCGAAAGCTTCATACGTCACTGTCAAGTTGCTCCAGGAGTTTGCACACTTGTCTATGGACCCAG	2671
CYP52A3B	2389	GCCTTGACTGAAGCTTCATACGTCACTGTCAAGTTGCTCCAGGAGTTTGGAAACTTGTCTCCCTGGATCCAA	2458
CYP52A5A	2510	GCCTTGACCGAAAGCTGGCTATGTGTGGTTAGATTGGTGCAAGAGTTCTCCACGTTAGGCTGGACCCAG	2579
CYP52A5B	2549	GCCTTGACCGAAAGCTGGTTACGTTTTGGTCAAGATTGGTGCAAGAGTTCTCCACACTTAGGCTGGACCCAG	2618
CYP52A8A	1856	GCTTTGACTGAAGCCGGTTACGTTTTGGTTAGACTTGTTCAGGAGTTTCCAAACTTGTCTACAAGACCCCG	1925
CYP52A8B	2409	GCTTTGACCGAAAGCCGGTTACGTTTTGGTTAGACTTGTTCAGGAAATTCCTTAGCTTGTACAGGACCCCG	2478
CYP52D4A	2120	GCAATCCTTGAAAGCTTCGTATGTTTTGGCTCGATTGACACACAGTGCTACACGACGATACAGCTTAG--AA	2186

FIG. 15H-3

CYP52A1A	2675	GTCTCGAATACCCCTCCACCAAGTGATTCACCTTGACCATGAGTCACCAACGATGGTGTCTTTTGTCAAGAT	2744
CYP52A2A	2691	ACACCGAATATCCACCTAAGAAAATGTCGCATTTGACCATGTGCTTTTCGACGGTGCCAATATTGAGAT	2760
CYP52A2B	2564	ACACCGAATATCCACCTAGGAAAATGTCGCATTTGACCATGTCCCTTTTCGACGGTGCCAACATTGAGAT	2633
CYP52A3A	2672	ACACCGAATATCCACCAAAAATTCAGAAACACCTTGACCTTGTGCTCTTTTGAATGGTGTGCTGATTAGAAAT	2741
CYP52A3B	2459	ACGCTGAGTACCCACCAAAAATTCAGAAACACCTTGACCTTGTCACTCTTTGATGGTGTGCTGACGTTAGAAAT	2528
CYP52A5A	2580	ACGAGGTGTACCCGCAAAAGAGGTTGACCAACTTGACCACTGTGTTTGCAGGATGGTGTCTATTGTCAAGTT	2649
CYP52A5B	2619	ATGAAGTGTATCCACCAAAAGAGGTTGACCAACTTGACCACTGTGTTTGCAGGATGGTGTCTATTGTCAAGTT	2688
CYP52A8A	1926	AAACCAAGTACCCACCACTAGATTGGCACACTTGACCATGTGCTTGTGTTGACGGTGACACACGTCACAGAT	1995
CYP52A8B	2479	AAACTGAGTACCCACCACTAGATTGGCACACTTGACCATGTGCTTGTGTTGACGGGGCATACGTCACAGAT	2548
CYP52D4A	2187	CTACCGAGTACCCACCAAGAACTCGTTTCATCTCAGCATGAGTCTTCTCAAACGGGGGTGTACATCCGAAC	2256
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CYP52A1A	2745	GTAA-AGTAGTCGATGCTGGGTATTCGATTACATGT--GTATAGGAAGATTTTGGTTTTTTTATTCTGTTCT	2811
CYP52A2A	2761	GTATTAGAGGGTCATGTGTTATTTT-GATTGTTA----GTTTGTAAATTACTGATTAGGTTAATTCAATG	2824
CYP52A2B	2634	GTATTAGAGGATCATGTGTTATTTTGTGTTAGTTGGTTAGTCTGTTGTAGCTATTGATTAGGTTAATTCACG	2703
CYP52A3A	2742	GTACTAAGGTTGCTTTTCCTTGCTAAATTTTCTCTGTATAGCTTGTGTATTAAATTGAATCGGCAATTG	2811
CYP52A3B	2529	GTTCTAAGGTTGCTTATCCTTGCTAGTGTATT--TATAGTTTGTGTATTAAATTGAATCGGCGATTG	2595
CYP52A5A	2650	TGACTAGCGCGGTGGAATGCGTTTGTGTTTGTGTA--GTTTCTGTTTGCAGTAATGAGATAACTATTCA	2716
CYP52A5B	2689	TGACTAGTA-CGTA-TGAGTGCCTTGTGTTTGTGTA--GTTTCTGTTTGCAGTAATGAGATAACTATTCA	2753
CYP52A8A	1996	GTCATAGGTTTCCC---CATACAAGTAGTTCAGTA--ATTATACACTGTTTTTACTTCTCTTCATACC	2059
CYP52A8B	2549	GCAATAGGTTT-----TGGTTTGACTTTGTTTCCATA--	2580
CYP52D4A	2257	TAGAACTTGATTATGTTTATGTTTAAATCGGGGCAAGCACTGCAAGTCATTGATGTTTGTGGAAGCCCC	2326

FIG. 15I-I

CYP52A1A	2812	TTTTTTTAAATTTTGTGTTAAATTAG-TTTAGAGATTTCATTAAATACATAGATGGGTGCTATTTCGAAACT	2880
CYP52A2A	2825	GATTGTTATTATTGATAGGGTT-----TGCGGTGTTGCATTCACTTGGGATCGTTCCAGGTTG	2885
CYP52A2B	2704	GATTGTTATTATTGATAGGGGTGCGTGTGTGTGTTGCATTACATGGGATCGTTCCAGGTTG	2773
CYP52A3A	2812	ATTTTCTGATACCAATAAACCGTA-----GTGCGATTGACCAAAACCGTTCAAAAGTTTGTGTTCTC	2873
CYP52A3B	2596	ATTTTCTGTTACTAATAACTGTA-----GTGGGTTTGTACCAAAACCGTTCAAAAGTTTGTGTTCTC	2657
CYP52A5A	2717	GATAAGGCGAGTGGATGTACGTTT-TGTAAGAGTTT-CCT-TACAACCTTGGTGGG-TGTGTGAGGTT	2781
CYP52A5B	2754	GATAAGGCGGTGGATGTACGTTT-TGTAAGAGTTT-CCT-TACAACCTTGGTGGG-TGTGTGAGGTT	2817
CYP52A8A	2060	AAATGGACAAAAGTTTAAAGCATG-CCTAACACGTGACCG-GACAATTGTGTGCGCCTAGTATGTAACA	2127
CYP52A8B	2581	-----TGCAAGT	2587
CYP52D4A	2327	AGCATTGGTGTTCGGAGCATCAATAACCAATGTCTTGAAGGTTTGTGATTTCCTTGACCTTCTTCTTCTCT	2396
CYP52A1A	2881	TTACTTCTATCC--CCTGTATCCCTTATTATCCCTCTCAGTCACATGATTGCTGTAATTGTCGTGCAGGA	2948
CYP52A2A	2886	ATGTTTCCTTCCATCCT--GTCGAGTCAAAAGGAGTTTGTGTTGTAACTCCGGACGATGTTTAAATAG	2953
CYP52A2B	2774	TTGTTTCCTTCCATCCT--GTTGAGTCAAAAGGAGTTTGTGTTGTAACTCCGGACGATGCTTTAGATAG	2841
CYP52A3A	2874	TCGTTGACG-----TGCTCGCTCATCAGCACTGTTTGAAGACGAAAGA-GAAAAATTTTGTGTA	2930
CYP52A3B	2658	TTTCTTCCCTACCTTCGTTGCTCGCTCATCAGCACTGTTTGAACGAAAAAGAAAAATTTTGTGTA	2727
CYP52A5A	2782	GAGTTGTCATCTT-GGGGAGATTACACCTTTTG-CAGCTCTCCGTATACACTTGTACTCTTTGTAAACCTC	2849
CYP52A5B	2818	G----CATCTTAG-GGAGAGATAGCACCTTTTG-CAGCTCTCCGTATACAGTTTACTCTTTGTAAACCTA	2881
CYP52A8A	2128	ATTGTAATAAATAG-TGTACACTAATTGTGGTGGCCGGAGATAAATTACAGTTTGTGTTGTGTAACCTC	2196
CYP52A8B	2588	AGTTCAGTAAT---TACACACTAATTGTGGTGGCCGGGATAAATTACCGTTTGTGTTGTGTAATAAT	2654
CYP52D4A	2397	GAGCTTCTTTCCG--TCAAACTTGACAGAAATGGCCATCATTTACAGGAACAACCA-CGTACGACGGCCGG	2463

FIG. 15I-2

CYP52A1A	2949	CACAACTCCCTAACGGACTTAAACCATATAACAAGCTCAGAACCATAGCCGACATCACTCCTTCTTCTC	3018
CYP52A2A	2954	AAGGTCGATCTCCATGTGATTGTTTGTACTGTGATTATGTAATCTGCG-----GACGTTATA	3016
CYP52A2B	2842	AAGGTCGATCTCCATGTGATTGTTT-GACTGCTACTCTGATTATGTAATCTGTAAAGCCTAGACGTTATG	2910
CYP52A3A	2931	AACAACACTGTCCAAATTTACCCCAACGTGAACCATATG--CAAATGAGCGGCC-----CTTTCAA	2989
CYP52A3B	2728	AACAACATTGCCCAAACTTACCCCAACGTGAACCATATAACCAAAATGAGCGGCG-----CTTTCAA	2788
CYP52A5A	2850	TATCAATCATGTGGGGGGGGGTTCAATTGTTTGGC-CATGGTGGTGCAATGTTAAATCCGCC-AACTACC	2917
CYP52A5B	2882	TGCCAATCATGTGG-----GGATTCAATTGTTGCC-CATGGTGGTGCAATGCAAAATCCCCCAACTACC	2944
CYP52A8A	2197	GCGGATATCTCTGGC-----AGTTTCTCTTCTCCGC-AGCAGCTTTGCCACGGGTTTGCTCTGGGGCCAA	2260
CYP52A8B	2655	TCGGACATCTCTGGT-----GGTTTCCCTTCTCCGC-AGCAGCTTTGCCACGGGTTTGCTCTGGGGCCAA	2718
CYP52D4A	2464	TACCGCATCTGGAGTA---TCTCGCCGTCGTTCAAGTAG--CACGAAACAGCAACGACGTCAACCATCTG	2528

FIG. 15I-3

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FIG. 15J-1

CYP52A1A	3159	GTCCAAAGACGGCGAGTTCTGGTGTGCCCCGGAATCAGCCATCCCGGCCACATACAAGCAGCCGTTGATT	3228
CYP52A2A	3145	CAAAAAATGGGAAACTC--CAACAGACAAAA-AAAAAACTCCGAGCACTCCGAAACCCACAGAAACAATG	3211
CYP52A2B	3044	CAAAAGATGAGAAACTC--CAACAGAAAAAATAAAAAAATCCGAGCACTCCGAAACCAACAAAAACAATG	3111
CYP52A3A	3120	GAAGAATCAGCCAGA---AACTAGCGATGGATCCAAAGCCTGTGACCTTGCCCAATGGAGACGAAGTG	3185
CYP52A3B	2919	GAAGAATCGCGCCAGA---AACTAGCGATGGATCCAAAGCCTGTGGCCTTGCCCAATGGAGACGAAGTG	2984
CYP52A5A	3055	AGACAACCCAGAAAAAAGAAACAAATCCAGATAGAAAAACAAAGGGCT-GGACAACCATATAAT-AAAC	3122
CYP52A5B	3074	AGACAACCCAGAAAAA-----CAAAATCCAGATAGAAAGAAAGGGCT-GGACAACCATATAAT-AAAC	3135
CYP52A8A	2387	TTATGTCTGAGGCGTG---CTTGAAAGAAGTGTCAAAATGTGACAGGCG-ACGCTATTCGACAT-GAAC	2450
CYP52A8B	2855	TTATGTCTAAGGCGTG---CTTGACACAAGTGTCAAAAGGTGACAGGCG-ACGTTATTCGACAT-GAAC	2918
CYP52D4A	2659	CCACCACTGCCCTCGG-----TTGAGTCAAGGCAGTATGATGCCCGGGATCCAGTACTCCAATGGGAACC	2722
CYP52A1A	3229	GCGTGCACTACTCGGCGAGCCCAAAATGGAGCCACGCAATCGGACCATGAAGCAAAAGTACATTCAACGAGA	3298
CYP52A2A	3212	GGG---CGCCAGAAATTATTGACTATTGTGACTTTTAA-----CGCTAACGCTCATTCAGTG	3266
CYP52A2B	3112	GGG--GCGCCAGAAATTATTGACTATTGTGACTTTTAA-----ATTTTTCCGTTAACTTTCATTGCAGTG	3177
CYP52A3A	3186	GAGTTGAACCAAGCGTTCCTAGAAGTTACCACATTAATGTGCAATGAGTTTGACTTGGACCAATTGAACG	3255
CYP52A3B	2985	GAGTTGAACCAAGCGTTCCTAGAAGTTACCACATTAATGTGCAACGAGTTTGACTTGGACCAATTGAACG	3054
CYP52A5A	3123	AATCTAGGGTCTACTCCATCTTCCACTGTTTCTTCTTCTTCAGACTTAGCT-AACAACAACACTCACTTCA	3191
CYP52A5B	3136	AACCTAGGGTCCACTCCATCTTCACT--TCTTCTTCTTCAGACTTATCT-AACAACGACTCACTTCA	3201
CYP52A8A	2451	GCGAAAGGGTTATTTGCATCAATACGAG--GGGCTGACTCTAGTCTAGG--ATGGCAGTCTTAGGTTGC	2515
CYP52A8B	2919	GCAAAAGGGTAATTTGCATCGATACGAG--GGGTGCTCTGGTCTAAG--AAGGACCCCCCAGGTTGC	2983
CYP52D4A	2723	TCT----GCACGGTGTGCTGCAGTTTGTAGGGCGTATTTCGA-----TCCATGATCGTTCCTTTGG	2779

FIG. 15J-2

CYP52A1A	3299	TCACGGGTGTTTCAG-TGTGCGAGATTGAGAAAGTTCGACGATGGATGGAAGTACGATCTCGTTGCGGATT	3367
CYP52A2A	3267	TAGTGGGTCTTACACGG-----GGTATTGCTTTCTACAATGCAAGGCA-CAGTTGAAGGTTTGCACC	3328
CYP52A2B	3178	AAGTGTGTTACACGGGGTGGTGATGGTGTGGTTTCTACAATGCAAGGCA-CAGTTGAAGGTTTCCACA	3246
CYP52A3A	3256	CGGCAGAGTTGTTTACTA-CGCTGGCGACATATCTACAAGAAGGGCACATCAATCGCAGACAGTGCCA	3324
CYP52A3B	3055	CGGCCGAGTTGTTTACTA-CGCCGGCGACATATCTACAAGAAGGGCACATCAATGCGACAGTGCCA	3123
CYP52A5A	3192	CCATGGATTACGCAGGCATCACGGGTGGTCCATCAGAGG-CGAGGCCCTTGAAGAACTCG--CAGAATT	3258
CYP52A5B	3202	CCATGGATTACGCAGGCATCACGGGTGGTCCATCAGAGG-CGAGGCCCTTGAAGAACTCG--CCGAGTT	3268
CYP52A8A	2516	AAACATGTTGCACCA-TATCCCTCCTGGAGTTGGTCGAC--CTCGCCTACGCC-ACCCTCA--GCGATCG	2579
CYP52A8B	2984	AAACATGTTGCACCTG-CATCCCACTCAGAGTTGGTCGAC--CACGCCCTACGCTTACCCTCA--GCGATCG	3048
CYP52D4A	2780	TGCTGTAGTATAACGAGCT--CTTGGTGTCTCTTGAAATGGAACAGGTTGGATGTGTGTTGAGTTTGTCT	2847

FIG. 15J-3

CYP52A1A	3368	ACGACTTCGGTGGGTTGTTATCTAAACGAAGATTCTATGAGACGCAGCATGTGTTTCGGTTCGAGGATTG	3437
CYP52A2A	3329	TAAAGTTGCCCGGTGTCAACTCAATTGAC-----G--AGTAACTTCCTAAGCTCGAATTATGCG	3385
CYP52A2B	3247	TAAAGTTGCACCATATCAACTCAATTATC-----CTCATTCATGTGATAAAAGAGAGCCAAA	3305
CYP52A3A	3325	GATTGTCTTATTATTGAGAGCAAACTAC-----ATCTTGAACATACCTTGGGTATTGAT	3379
CYP52A3B	3124	GATTGTCTTACTATTGAGAGCAAACTAC-----ATCTTGAACATACCTTGGGTACTTTAT	3178
CYP52A5A	3259	G-ACCATCCAGAACCCAGCCATCCAGCT-----TGAAAGAAATCAACACCGGCATCCAGAGGACGACTT	3321
CYP52A5B	3269	G-ACCATCCAGAACCCAGCCATCCAGCT-----TGAAAGAAATCAACACCGGCATCCAGAGGACGACTT	3331
CYP52A8A	2580	GCACCTTCCGTTGTTCAATATTCTC-----CTTCCCATTTGTTCCAGGGGTTA--TC	2629
CYP52A8B	3049	GCACCTTCCGTTGTTCAATATTCTCT-----CCCCCTGCTTCCCCCCCATTTGTTCCAGGGATTA--TC	3110
CYP52D4A	2848	GCGTGCTTGGTTTGCAAGTCTTCGATCG-----AGCGTAGTGAGTAGACAGTTGGCGGG	2901
CYP52A1A	3438	TGCGTACGTCATGAGTGTGCCCTTTTGATGGACCCAAAGGAGGAAAGTTACGTGTTGGGACGTACAGATCC	3507
CYP52A2A	3386	AGCT-CGTGCGTCAACCTATGTGCAGGAAAGAAATCCAAAAA--AATCGAAA-ATGCGACTTTCGAT	3451
CYP52A2B	3306	AGGT-AAT-TGCGAGACCCCCCAAGGGGAAACACGGAGTAGAAAGC--AATGGAAAACACGCCCATGACAGT	3371
CYP52A3A	3380	TTCG-AAGCAGGGATTGGATTGTGATAGTCACGGACAAACACGCGT--TGTTTGATAGTATTTTGAAAAAGT	3446
CYP52A3B	3179	TTCG-AAGCAGCGATTGGATGTGATAGTCACCGACAAACACGCGT--TGTTTGATAATATTTTGAAAAAGT	3245
CYP52A5A	3322	TGCC-AAGTTGTTGTCTGCCACCCCGAAAATCCCCACCAAGCACA--AGTTGAACGGCAACCCACGAATT-	3387
CYP52A5B	3332	TGCC-AAGTTGTTGTCTGCCACCCCGAAAATCCACACCAAGCACA--AGTTGAATGGCAACCCACGAATT-	3397
CYP52A8A	2630	AACA-ACGTTGCCGGCCTCCTC-----CCCAAATTA-----CAAGAAAAATAAAATT-	2674
CYP52A8B	3111	AACA-ACGTTGCCGGTCTCCTCTCCCCCCCCTCCCCCAGTTAT-----GTACAAGAAAAATTAAATT-	3171
CYP52D4A	2902	GGTGGTGCTCGGGCTTTATTCTGTGTTTGTGTTTCTCTTAGT--CTTGGAATGACGCTGTTATCGAC	2969

FIG. 15K-I

CYP52A1A	3508	ATTGAAAGGTTGAGCTGGGGTAAAGACGGGGACGTGGA-GTGGACCATGG---CGACGACGTGGGATCCT	3573
CYP52A2A	3452	TTTGAATAAACCAAAAGAAAAATGTCGCACCTTTTTC-----TCGCTCTCGCTCTCTCGACCCAAATCA	3516
CYP52A2B	3372	GCCATTTAGCCACA--ACACATCTAGTATTCTTTT-----TTTTTTTGTGCGAGGTGCACACCTGG	3433
CYP52A3A	3447	TTTGAAAAGATCTAC---AAGTTGATAAGCGTGTGA-----ACGATATGATTGACAAAGAAAGGTGA	3507
CYP52A3B	3246	TTTGAAAAGATCTAC---AAGTTGATAAGCGGTGA-----ACGATATGATTGACAAAGAAAGGTGA	3306
CYP52A5A	3388	GTCTGAGGTCGCCATTGCCAAAAGAGGTACGAGGTGTGATTGCCTTGAGCGACGCCACAAAAGACCCA	3457
CYP52A5B	3398	GTCCGAAGTCGCCATTGCCAAAAGAGGTACGAGGTGTGATTGCCTTGAGCGACGCCACAAAAGAACCA	3467
CYP52A8A	2675	GTGCGACGGCACCGATCTGTCAAAGATACAGATAA-----ACCTTAAATCTGCAAAAACAAGACCCC	2736
CYP52A8B	3172	GTGCGACGGCACCGATACGTCAAAGATACAGAGAA-----ACCTTAA-----TCC	3216
CYP52D4A	2970	GGTTCGTAGTATAAGTAGCGCCAATATGAGAATGTATA-----TCCGCATCACCCAAAGACTCTTCAGCCT	3034
CYP52A1A	3574	GGTGGGTTTATCCCGCA-ATGGATAACTCGATTGAGCA-TCCCTGGAGCAATCGCAAAAGATGTGCCTAG	3641
CYP52A2A	3517	CAACAAATCCTCGCGCGCAGTATTCGACGAAAC--CACAAACAATAAAAAACAATAATCTACACCACT	3584
CYP52A2B	3434	ACTTTAGTTATTGCCC-CATAAAGTTAAACAATCT--CACCTTTGGCTCTCCAGTGTCTCCGCCCTCCAGA	3500
CYP52A3A	3508	CAAGCGACATCAACAGTCTAGCATTCATCAATTG--CATCAACTACTCGAGAGGTCAACTATTCTCCGCA	3575
CYP52A3B	3307	CAAGCGACATCAACAGTCTAGCATTTATCAACTG--CATCAACTACTCGAGGGGTCAACTATTCTCCGCA	3374
CYP52A5A	3458	ATCAAAGTGACCTCCAGATCAAGATCTTGATTGACAAGTTCAAGGTGTAATTGT---TTGAGTTGCCTG	3524
CYP52A5B	3468	ATCAAAGTGACCTCCAGATCAAGATCTTGATTGACAAGTTCAAGGTGTAATTGT---TTGAGTTGCCTG	3534
CYP52A8A	2737	TCCCCATAGCCTAGAAGCACCAGCAAGATGATGGAGCAACTCTCCAGTACTGGTACATCGCACTCTCTG	2806
CYP52A8B	3217	CTCCCATAGCCTAGAAGCATCAAAAAGATGATTGAGCAACTCTCCAGTACTGGTACATTCGACTCCCTG	3286
CYP52D4A	3035	GTTACAACGACTGAGGCTGTTGGCCGTGTGACCAATTGGTTTCTTTGGTGACCTAGATTGGTCCCGCAGG	3104

FIG. 15K-2

CYP52A1A	3642	TG---	TATTAAACTACATACAGAAATAAAAACGTGTCTTGATTCATTGGTTT--GGTTCTTGTGGGTT	3705
CYP52A2A	3585	T----	CTTTTCTTCAACAGTCAACAAAAACAACAAATATACACCATTTCAACGATTTTGTCTCTTAT	3650
CYP52A2B	3501	TG---	CTCGTTTACACCCCTCGAGCTAACGACAAACAACCCATGAGGGGAATGGGCAAGTT-----	3562
CYP52A3A	3576	CA---	CGAACTTTTGGG-ACTGGTTTGTGTGGATTGGTCGACATCTATTTCAACCAAGTTTGGCACATTA	3641
CYP52A3B	3375	CA---	CGAACTTTTGGG-ACTGGTTTGTGTGGATTGGTTGACAACTATTTCAACCAAGTTTGGCTCATTA	3440
CYP52A5A	3525	AC---	CAGAAAGTTCTCCTACTCCATCGTGTCCTCAACTCCGTTAAACATTCGCCCCC-TGGACCTTGTCTCGGG	3590
CYP52A5B	3535	AC---	CAGAAAGTTCTCCTACTCCATCGTGTCCTCAACTCCGTTAAACATTCGCCCCC-TGGACCTTGTCTCGGTG	3600
CYP52A8A	2807	TA---	TGGTTTCATCCTTCGCTACTTGGCTTCCCACGCACGAGCCGCTACTTG-CGCCACAAGCTCGGCG	2872
CYP52A8B	3287	TA---	TGGTTTCATCCTTCGCTACTTGGCTTCCCACGCACGAACTTACTTG-CGCCACAAGCTCGGCG	3352
CYP52D4A	3105	GAAAGCAAGGCTGCTAGGGGGGCATACCAACAAGGTCGTGTAAATCAGTATCTATGGTGCTACCATGTG		3174

FIG. 15K-3

CYP52A1A	3706	CCGAGCCAAATATTTCACATCATCTCTCTAAATTTCTCAAGAATCCCAACGTAGCGTAGTCCAGCACGCCCT	3775
CYP52A2A	3651	AAATGCTATATAATGGTTTAAATTCAACTCAGGTATGTTTAT-TTTACTGTTTTTCAGCTCAAGTATGT--T	3717
CYP52A2B	3563	AAACACTTTTGGTTTCAATGATTCCTATTGCTACTCTCTTGTGTTTGTGTTTTGATTTGCACCATGT--G	3630
CYP52A3A	3642	GACAACTACAAGAAAGGTATTGGCATTTGATCTGAAGAACATCAGCGATGAAGACATCTTGATCATAC--A	3709
CYP52A3B	3441	GACAACTACAAGAAAGTATTGGCATTTGATCTGAAGAACATCAGTGAAGATATCTTGATCGTAC--G	3508
CYP52A5A	3591	AGAAAGTTGACCCAGGGCTTGATCAACTTGGCCTTCAGAGAACAAAGCAGCACTTGGACGAGGTCAATT-G	3659
CYP52A5B	3601	AGAAAGTTGACCCAGGGCTTGATCAACTTGGCGTTCAGAGAACAAAGCAGCACTTGGACGAGGTCAATC-G	3669
CYP52A8A	2873	CGGCGCCATTACGCAACACCCAGTACGACGGCTGGTATGGTTCAAGTTTGGCGGGAGTTTCTCAA--G	2940
CYP52A8B	3353	CGGCGCCGTTACGCAACACCCAGTACGACGGATGGTATGGTTCAAGTTTGGCGGGAGTTTCTCAA--G	3420
CYP52D4A	3175	TGTGTTGGGGGAAATTTCCCGCATTTTGTGTAAACGAAAGTTCTAGAAAGTTCTCGTGGGTTCTGAG-A	3243
CYP52A1A	3776	CTGAGATCTTATTAAATATCGACTTCTCAACCACCGGTGGAATC--CCGTTCAGACCATTTGTACCTGTA	3843
CYP52A2A	3718	CAAAATACTAACTACTTTTGATGTTTGTGCTTTTCTAGAATCAAAACAACGCCCAACAACACGCCGAGCTT	3787
CYP52A2B	3631	AAATAAACGACAAATTATATATACCTTT--TCGTCTGTCTC-----CAATGTCT-CTTTTGTGCTGCCATT	3692
CYP52A3A	3710	CTTCCTCCCATCGACACTACAATTGTTTAAGCTGGTGTGGACAA-GAAAGACGACGCTGCAGTTGAACA	3778
CYP52A3B	3509	CTTCCTCCCATCGACACTACAATTGTTTAAGCTGGTGTGGATAA-GAAAGACGACGCCACTGTTGACCA	3557
CYP52A5A	3660	ACATCTTCAACGAGTTTCATCGACAAGTTCTTTGGCAACACGGAG--CCGCAATTGAC-----CAACTTCT	3722
CYP52A5B	3670	ACATCTTCAACGAGTTTCATCGACAAGTTCTTTTGGCAACACAGAG--CCGCAATTGAC-----CAACTTCT	3732
CYP52A8A	2941	GCGAAGAAGATCGGGGGCAGACGGACTTGGTGCAATGCGCGGTT--CCGTGGCGG-----CATGGACA	3001
CYP52A8B	3421	GCGAAGAAGATTGGAAGGCAGACGGACTTGGTGCAATGCGCGGTT--CCGTGGAGGGG-----CATGGATA	3484
CYP52D4A	3244	ATCTGCTGGAACCATCCACCCGCATTTCCGTTGCCAAAGTGGAA-GAGCAATCAACCCACCCTGCTTTG	3312

FIG. 15L-1

CYP52A1A	3844	GTGTGTTTGCTCTTGTGATGACAAATGATGTATTTGTACGATACCTGAAATAATAAAACATCCAGT	3913
CYP52A2A	3788	GTCGAAATAGACGGTTTGTCTTACTCATTAGATGGTCCAGATTACTTTTCAAGCCAAAGTCTCT-CGAGTT	3856
CYP52A2B	3693	TTGCTTTTGTGCTTTTGTGCTTTTGCACT---CTCTCCCACTCCCACAATCAGTGCAGCAACACA-CAA	3755
CYP52A3A	3779	GTTCTACAAGTACATCACTTCAACAGT--GTCACGAGACTACAACTCCAACATCGGCTCCACAGCCAAAG	3846
CYP52A3B	3578	GTTCTACAAGTACATCACTTCAACAGT--GTCGCAAGACTACAACCTCCAACATCGGAGCCACAGCCAAAG	3645
CYP52A5A	3723	TGACCTTGTGCGGTGTGTGGACGGGTGATTGACCATGCC-AACTTCTTGAGCGTGTCTCGCGGACCT	3791
CYP52A5B	3733	TGACCTTGTGCGGTGTGTGGACGGGTGATTGACCATGCC-AACTTCTTGAGCGTGTCTCGCGGACCT	3801
CYP52A8A	3002	CTTCTCGAGCTACACTTTTCGGCATCCATATCATCTTACC-CGGGACCCGGAGAACATCAAGCGGTCT	3070
CYP52A8B	3485	CTTCTCGAGCTATACTTTTCGGCATCCATATCATCTTACT-CGGGACCCGGAGAACATCAAGCGGTCT	3553
CYP52D4A	3313	CCCAATCAGCCATTCCCCCTGGGAATATAAATTCAAC	3348
CYP52A1A	3914	CATTGAGCTTATTACTCGTGAACCTTATGAAAGAACTCATTCAGCCGTTCCCAAAAAACCCAGAAATTGAA	3983
CYP52A2A	3857	TTGTTTGCTGTTTCCCCCAATTCCCTAACTATGAAGGGTTTTTATAAGGTCCAAAGACCCCAAGGCATAGTT	3926
CYP52A2B	3756	ATGATATCGATTTGTCCAAAACCCAAACTCAGTGGCTTTTGAGGTGTGTGACGAGTT	3755
CYP52A3A	3847	ATGATATCGATTTGTCCAAAAGCC	3900
CYP52A3B	3646	TCAAAGATCTTCTTGAACCTTGGA CTGGTATGTGGAC	3663
CYP52A5A	3792	TCAAAGATCTTCTTGAACCTTGGA CTGGTATGTGGAC	3826
CYP52A5B	3802	TGCGGACGCAGTTCGATGACTTCTCGCTCGGTGGCAGGATCAGGTTCTTGAAGCCGTTGTTGGGGTATGG	3871
CYP52A8A	3071	TGCGGACGCAGTTCGATGACTTCTCGCTCGGTGGCAGGATCAGGTTCTTGAAGCCGTTGTTGGGGTATGG	3140
DYP52A8B	3554	TGGCGACGCAGTTCGATGACTTTTTCG	3579
CYP52D4A	3349		3348

FIG. 15L-2

CYP52A1A	3984	GATCTTGCTCAACTGGTCA	4053
CYP52A2A	3927	TGCAAGTAGTAGATCGCCATGATCTGATACTTTACCAAGCTATCCTCTCCA	3948
CYP52A2B	3756	TTTTTGGTTCCCTTCTTGTCGTG	3755
CYP52A3A	3901		3900
CYP52A3B	3669		3668
CYP52A5A	3827		3826
CYP52A5B	3872	CGACTTTTGTACGACGAGCCGACGAGTACCAGAACTT	3910
CYP52A8A	3141	GATATTCACGTT	3152
CYP52A8B	3580		3579
CYP52D4A	3349		3348

FIG. 15L-3

CYP52A1A	4054	AGTTCTCCACGTACGGCAAGTACGGCAACGAGCTCTGGAAGCTTTGTTGTTTGGGGTCATA	4115
CYP52A2A	3949		3948
CYP52A2B	3756		3755
CYP52A3A	3901		3900
CYP52A3B	3669		3668
CYP52A5A	3827		3826
CYP52A5B	3911		3910
CYP52A8A	3153		3152
CYP52A8B	3580		3579
CYP52D4A	3349		3348

FIG. 15M

CYP52A1A	1	MATQEI	IDS	VL	PYL	-----	TKWY	TV	ITAA	VL	FL	IST	NI	KNYV	38														
CYP52A2A	1	MTVHD	I	IATY	-----	FTKW	YV	IV	PL	AL	IAYR	VL	DY	FYGRY	35														
CYP52A2B	1	MTAQD	I	IATY	-----	ITKW	YV	IV	PL	AL	IAYR	VL	DY	FYGRY	35														
CYP52A3A	1	MSSSP	FA	QAE	VL	ATT	SPY	IE	YF	LD	NY	TR	WY	YF	IP	LV	LL	S	NF	I	S	L	L	H	TR	Y	50		
CYP52A3B	1	MSSSP	FA	QAE	VL	ATT	SPY	IE	YF	LD	NY	TR	WY	YF	IP	LV	LL	S	NF	I	S	L	L	H	TR	Y	50		
CYP52A5A	1	MIEQ	L	L	EY	-----	WY	VV	P	V	L	Y	I	K	Q	L	L	A	Y	T	K	T	R	V	30				
CYP52A5B	1	MIEQ	I	L	EY	-----	WY	I	V	P	P	V	L	Y	I	K	Q	L	A	Y	S	K	T	R	V	30			
CYP52A8A	1	MLDQ	I	L	H	Y	-----	WY	I	V	P	L	L	A	I	N	Q	I	V	A	H	V	R	T	N	Y	30		
CYP52A8B	1	MLDQ	I	F	H	Y	-----	WY	I	V	P	L	L	V	I	K	Q	I	V	A	H	A	R	T	N	Y	30		
CYP52D4A	1	MAIS	L	L	S	W	D	-----	V	I	C	V	F	I	C	V	C	V	F	G	Y	E	Y	C	Y	T	K	Y	32

CYP52A1A	39	KAKKLCVDP	P	P	Y	L	K	D	A	G	L	T	G	I	L	S	L	A	A	I	K	A	K	N	D	G	R	L	A	N	F	A	D	---	E	V	F	D	E	Y	85			
CYP52A2A	36	LMYKLGAKP	F	F	F	F	F	F	F	K	Q	T	D	C	F	G	F	K	A	P	L	E	L	L	K	K	S	D	G	T	L	I	D	F	T	L	---	Q	R	I	H	D	L	82
CYP52A2B	36	LMYKLGAKP	F	F	F	F	F	F	F	K	Q	T	D	C	F	G	F	K	A	P	L	E	L	L	K	K	S	D	G	T	L	I	D	F	T	L	---	E	R	I	Q	A	L	82
CYP52A3A	51	LERRFHAKP	L	G	N	F	V	R	D	P	T	F	G	I	A	T	P	L	L	I	Y	L	K	S	G	T	V	M	K	F	A	W	G	L	N	N	K	Y	I	V	100			
CYP52A3B	51	LERRFHAKP	L	G	N	V	L	D	P	T	F	G	I	A	T	P	L	L	I	Y	L	K	S	G	T	V	M	K	F	A	W	S	F	N	N	K	Y	I	V	100				
CYP52A5A	31	LMKKLGAAP	V	T	N	K	L	Y	D	N	A	F	G	I	V	N	G	W	K	A	L	Q	F	K	K	E	G	R	A	Q	E	Y	N	---	Y	K	F	D	H	S	77			
CYP52A5B	31	LMKQLGAAP	I	T	N	L	Y	D	N	V	F	G	I	V	N	G	W	K	A	L	Q	F	K	K	E	G	R	A	Q	E	Y	N	---	H	K	F	D	S	S	77				
CYP52A8A	31	LMKKLGAKP	F	T	H	V	Q	R	D	G	W	L	G	F	K	F	G	R	E	F	L	K	A	S	A	G	R	L	V	D	L	I	---	S	R	F	H	D	N	77				
CYP52A8B	31	LMKKLGAKP	F	T	H	V	Q	L	D	G	W	F	G	F	K	F	G	R	E	F	L	K	A	S	A	G	R	V	D	L	I	---	S	R	F	H	D	N	77					
CYP52D4A	33	LMHKGAREI	E	N	V	I	N	D	G	F	F	G	F	R	L	P	L	L	M	R	A	S	N	E	G	R	L	I	E	F	S	V	---	K	R	F	E	S	A	79				

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CYP52A1A	86	PN--HTFYLSVAGALKIVMTVDPENIKAVLATQFTDFSLGTRHAFAPLL	133
CYP52A2A	83	DRPDIPTFTFPVFSINLVNTLEPENIKAILATQFNDFSLGTRHSHFAPLL	132
CYP52A2B	83	NRPDIPTFTFPFISINLISTLEPENIKAILATQFNDFSLGTRHSHFAPLL	132
CYP52A3A	101	RDPKYTTGLRIVGLPLIETMDPENIKAVLATQFNDFSLGTRHDFLYSLL	150
CYP52A3B	101	KDPKYTTGLRIVGLPLIETIDPENIKAVLATQFNDFSLGTRHDFLYSLL	150
CYP52A5A	78	KNPSVGTYSILFGTRIVVTKDPENIKAILATQFGDFSLGKRHTLTKPPLL	127
CYP52A5B	78	KNPSVGTYSILFGTKIVVTKDPENIKAILATQFGDFSLGKRHALFKPPLL	127
CYP52A8A	78	ED----TFSSYAFGNHVFTTRDPENIKALLATQFGDFSLGSRVKKFKPPLL	123
CYP52A8B	78	ED----TFSSYAFGNHVFTTRDPENIKALLATQFGDFSLGSRVKKFKPPLL	123
CYP52D4A	80	PHPQNTLVNRALSVPVILTDPVNIKAMLSQFDDFSLGLRLHQFAPLL	129
		.. * * * * * * * * * * * * * *	
CYP52A1A	134	GDGIFTLDGEGWKHSRMLRPQFARDQIGHVKALEPHIQIMAKQIKLNQG	183
CYP52A2A	133	GDGIFTLDGAGWKHSRMLRPQFAREQISHVKLLEPHVQVFFKHVRKAQG	182
CYP52A2B	133	GDGIFTLDGAGWKHSRMLRPQFAREQISHVKLLEPHMQVFFKHVRKAQG	182
CYP52A3A	151	GDGIFTLDGAGWKHSRTMLRPQFAREQSHVKLLEPHVQVFFKHVRKHRG	200
CYP52A3B	151	GDGIFTLDGAGWKHSRTMLRPQFAREQSHVKLLEPHVQVFFKHVRKHRG	200
CYP52A5A	128	GDGIFTLDGEGWKHSRMLRPQFAREQVAHVTSLEPHFQLLKKHILKHKG	177
CYP52A5B	128	GDGIFTLDGEGWKHSRMLRPQFAREQVAHVTSLEPHFQLLKKHILKHKG	177
CYP52A8A	124	GYGIFTLDAEGWKHSRMLRPQFAREQVAHVTSLEPHFQLLKKHILKHKG	173
CYP52A8B	124	GYGIFTLDGEGWKHSRMLRPQFAREQVAHVTSLEPHFQLLKKHILKHKG	173
CYP52D4A	130	GKGIFTLDGPEWKQSRMLRPQFAKDRVSHILDLEPHFVLLRKHIDHNG	179
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FIG. 16A-2

CYP52A1A	184	KTFDIQELFFRFTVDTATEFLFGESVHSLYDEKLGITP-NEIPGRENFA	232
CYP52A2A	183	KTFDIQELFFRLTVDSATEFLFGESVESLRDESIGMSINALDFDGKAGFA	232
CYP52A2B	183	KTFDIQELFFRLTVDSATEFLFGESVESLRDESIGMSINALDFDGKAGFA	232
CYP52A3A	201	QTFDIQELFFRLTVDSATEFLFGESAESLRDESIGLPTTKDFDGRRDFA	250
CYP52A3B	201	QTFDIQELFFRLTVDSATEFLFGESAESLRDDSVGLTPTTKDFEGRGDFA	250
CYP52A5A	178	EYFDIQELFFRFTVDSATEFLFGESVHSLKDESIGINQDDIDFAGRKQFA	227
CYP52A5B	178	EYFDIQELFFRFTVDSATEFLFGESVHSLKDETINGINQDDIDFAGRKQFA	227
CYP52A8A	174	EYFDIQELFFRFTVDSATEFLFGESVHSLKDEEIGYDTKDMSEERRR-FA	222
CYP52A8B	174	EYFDIQELFFRFTVDSATEFLFGESVHSLRDEEIGYDTKDMAEERRK-FA	222
CYP52D4A	180	DYFDIQELYFRFMSMDVATGFLFGESVGSGLKDE-----D-----ARFL	216
		***** ** . * ** ***** ** * *	
			*
CYP52A1A	233	AAFNVSQHYLATRSYSQTFYFLTNPKEFRDCNAKVHHLAKYFVNKALNFT	282
CYP52A2A	233	DAFNYSQNYLASRAVMQQLYWVLNGKKFKECNAKVHKFADYYVVKALDLT	282
CYP52A2B	233	DAFNYSQNYLASRAVMQQLYWVLNGKKFKECNAKVHKFADYYVVKALDLT	282
CYP52A3A	251	DAFNYSQTYQAYRFLQMQYWI L NGSEFRKSI AVHKFADHYVQKALELT	300
CYP52A3B	251	DAFNYSQTYQAYRFLQMQYWI L NGAEFRKSI AVHKFADHYVQKALELT	300
CYP52A5A	228	ESFNKAQEYLAIRTLVQTFYWLNNKEFRDCTKL VHKTNYVYVQKALDAS	277
CYP52A5B	228	ESFNKAQEYLSIRILVQTFYWLNNKEFRDCTKL VHKTNYVYVQKALDAT	277
CYP52A8A	223	DAFNKSQVYVATRVALQNLWLVNNKEFECNDI VHKTNYVYVQKALDAT	272
CYP52A8B	223	DAFNKSQVYLSSTRVALQTLWLVNNKEFECNDI VHKTNYVYVQKALDAT	272
CYP52D4A	217	EAFNESQKYLATRATLHELHYFLCDGFRFRQYNKVVRKFCSCQCVHKALDVA	266
		*** . * * . * . * . * . * . * . * . * . * . * . *	

FIG. 16B-I

CYP52A1A	283	PEELEKSKSGYVFLYELVKQTRDPKVLQDQQLNIMVAGRDTTAGLLSFA	332
CYP52A2A	283	PEQLE-K-QDGYVFLYELVKQTRDKQVLRDQQLNIMVAGRDTTAGLLSFV	330
CYP52A2B	283	PEQLE-K-QDGYVFLYELVKQTRDRQVLRDQQLNIMVAGRDTTAGLLSFV	330
CYP52A3A	301	DDDLQ-K-QDGYVFLYELAKQTRDPKVLQDQQLNIMVAGRDTTAGLLSFV	348
CYP52A3B	301	DDDLQ-K-QDGYVFLYELAKQTRDPKVLQDQQLNIMVAGRDTTAGLLSFV	348
CYP52A5A	278	PEELE-K-QSGYVFLYELVKQTRDPNVLRDQSLNILLAGRDTTAGLLSFA	325
CYP52A5B	278	PEELE-K-QGGYVFLYELVKQTRDPKVLQDQSLNILLAGRDTTAGLLSFA	325
CYP52A8A	273	PEELE-K-QGGYVFLYELVKQTRDPKVLQDQSLNILLAGRDTTAGLLSFA	320
CYP52A8B	273	PEELE-K-QGGYVFLYELAKQTKDPNVLRDQSLNILLAGRDTTAGLLSFA	320
CYP52D4A	267	PEDTS----EYVFLRELVKHTRDPVVLQDQALNVLLAGRDTTASLLSFA	311
		**** *	
CYP52A1A	333	LFELARHPMWSKLREEIEVNFVGEDSRVEEITFEALKRCEYLKAILNE	382
CYP52A2A	331	FFELARNPEVTNKLREEIEDKFGLGENASVEDISFESLKSCEYLKAVLNE	380
CYP52A2B	331	FFELARNPEVTNKLREEIEDKFGLGENARVEDISFESLKSCEYLKAVLNE	380
CYP52A3A	349	FYELSRNPEVFAKLREEEVENRFGLGEEARVEEISFESLKSCEYLKAVINE	398
CYP52A3B	349	FYELSRNPEVFAKLREEEVENRFGLGEEARVEEISFESLKSCEYLKAVINE	398
CYP52A5A	326	VFELARHPEIWA KLREEIEQQFGLGEDSRVEEITFESLKRCEYLKAFLE	375
CYP52A5B	326	VFELARNPHIWA KLREEIEQQFGLGEDSRVEEITFESLKRCEYLKAFLE	375
CYP52A8A	321	VFELARNPHIWA KLREEIEQQFGLGEDSRVEEITFESLKRCEYLKAVLNE	370
CYP52A8B	321	VFELARNPHIWA KLREEIESHFGLGEDSRVEEITFESLKRCEYLKAVLNE	370
CYP52D4A	312	TFELARNDHMRKLREEVILTMGPSSD-----EITVAGLKSCRYLKAILNE	357
		***. *	

FIG. 16B-2

CYP52A1A	383	TLRMYPSPVNFRTATRDTTLPRGGGANGTDPIYIPKGSTVAYVVYKTHR	432
CYP52A2A	381	TLRLYPSVPQNFRTATKNTTLPRGGKDGSLPVLVRKGQTVIYGVYAAHR	430
CYP52A2B	381	TLRLYPSVPQNFRTATKNTTLPRGGKDGSLPVLVRKGQTVMYGVYAAHR	430
CYP52A3A	399	TLRLYPSVPHNFRTATKNTTLPRGGGEDGYSPIVVKKGQVVMYTVIATHR	448
CYP52A3B	399	ALRLYPSVPHNFRTATKNTTLPRGGKDGCSPIVVKKGQVVMYTVIGTHR	448
CYP52A5A	376	TLRIYPSVPRNFRTATKNTTLPRGGGSDGTSPILIQGEAVSYGINSTHL	425
CYP52A5B	376	TLRVYPSVPRNFRTATKNTTLPRGGGPDGTQPIILIQGEGVSYGINSTHL	425
CYP52A8A	371	TLRLHPSVPRNARFAIKDNTTLPRGGGPNKGKDPILIRKDEVVQYSISATQT	420
CYP52A8B	371	TLRLHPSVPRNARFAIKDNTTLPRGGGPNKGKDPILIRKNEVVQYSISATQT	420
CYP52D4A	358	TLRLYPSVPRNARFATRNNTTLPRGGGPDGSFPILIRKGQVPVGYFICATHL	407
		.. ** * * * * * * * * * * * * * * * * *	
CYP52A1A	433	LEYYGKDANDFRPERWFEPSTKLGWAYVVPFNGGPRVCLGQQFALTEAS	482
CYP52A2A	431	NPAVYGKDALEFRPERWFEPETKLGWAFLPFNGGPRICLGQQFALTEAS	480
CYP52A2B	431	NPAVYGKDALEFRPERWFEPETKLGWAFLPFNGGPRICLGQQFALTEAS	480
CYP52A3A	449	DPSIYGADADVFRPERWFEPETKLGWAYVVPFNGGPRICLGQQFALTEAS	498
CYP52A3B	449	DPSIYGADADVFRPERWFEPETKLGWAYVVPFNGGPRICLGQQFALTEAS	498
CYP52A5A	426	DPVYGGPDAAEFRRPERWFEPSTKLGWAYLPFNGGPRICLGQQFALTEAG	475
CYP52A5B	426	DPVYGGPDAAEFRRPERWFEPSTKLGWAYLPFNGGPRICLGQQFALTEAG	475
CYP52A8A	421	NPAYYGADAADFRPERWFEPSTRNLGWAFLPFNGGPRICLGQQFALTEAG	470
CYP52A8B	421	NPAYYGADAADFRPERWFEPSTRNLGWAFLPFNGGPRICLGQQFALTEAG	470
CYP52D4A	408	NEKVYGNDSHVFRPERWAALGKSLGWSYLPFNGGPRSCLGQQFAILEAS	457
		** * * * * * * * * * * * * * * * * *	

FIG. 16C-I

CYP52A1A	483	YVITRLAQMFETVSSDPGLEYPKCIHLTMSHNDGVFKM	523
CYP52A2A	481	YVTVRLVQEFHLSMDPDTEYPPKMSHLTMSLFDGANIEM	522
CYP52A2B	481	YVTVRLVQEFHLSMDPDTEYPPKMSHLTMSLFDGANIEM	522
CYP52A3A	499	YVTVRLVQEFHLSMDPDTEYPPKQNTLTSLFDGADVRMY	540
CYP52A3B	499	YVTVRLVQEFHLSMDPDTEYPPKQNTLTSLFDGADVRMF	540
CYP52A5A	476	YVLVRLVQEFHLSMDPDTEYPPKRLTNLTMCQDGAIVKFD	517
CYP52A5B	476	YVLVRLVQEFHLSMDPDTEYPPKRLTNLTMCQDGAIVKFD	517
CYP52A8A	471	YVLVRLVQEFHLSMDPDTEYPPKRLTNLTMCQDGAIVKMS	512
CYP52A8B	471	YVLVRLVQEFHLSMDPDTEYPPKRLTNLTMCQDGAIVKMQ	512
CYP52D4A	458	YVLARLTQCYTTIQLR-TTEYPPKKLVHLTMSLLNGVYIRTRT	499

** ** * . . . ** * . . . *

FIG. 16C-2

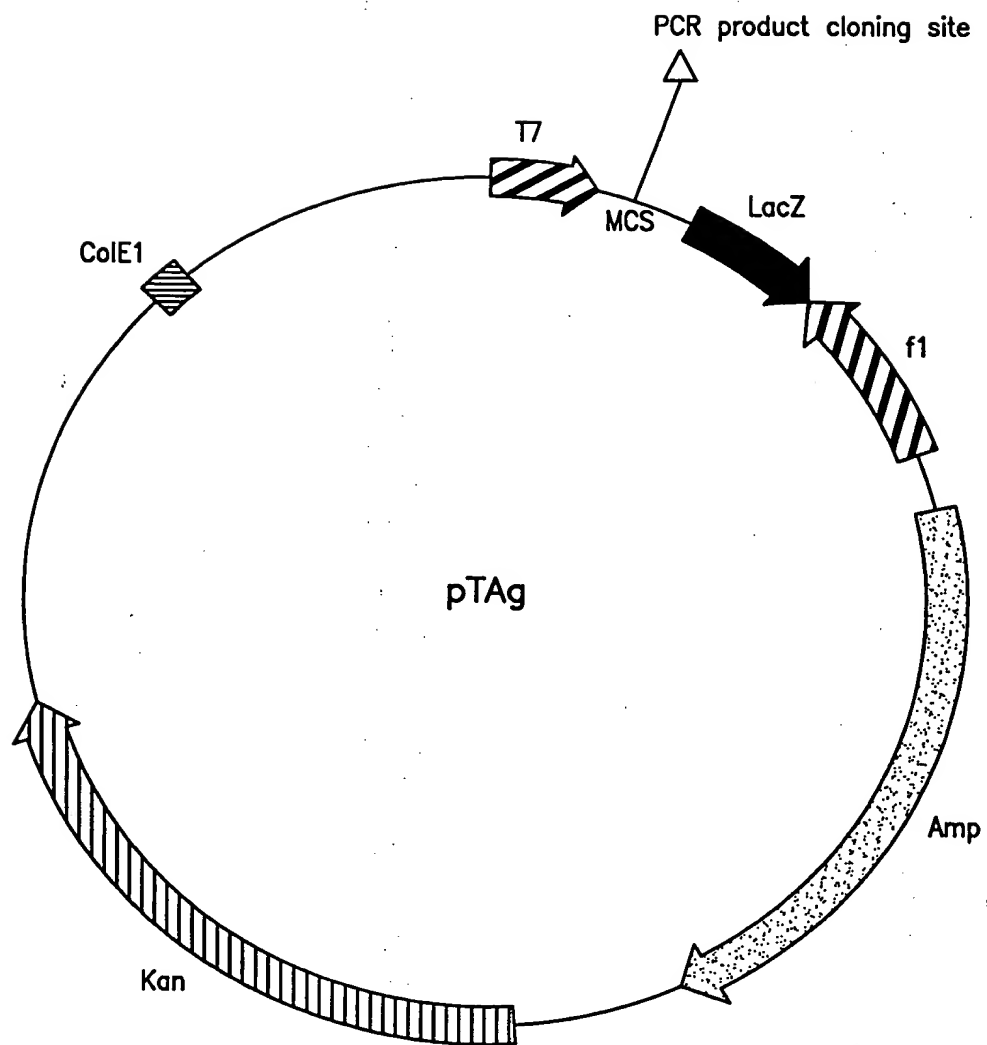
[illegible]

FIG. 17

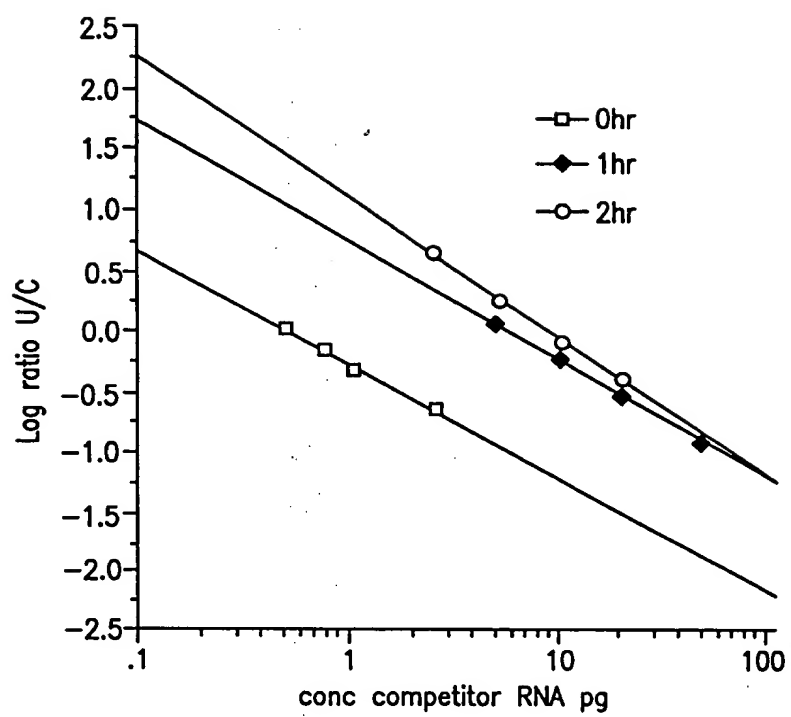


FIG. 18

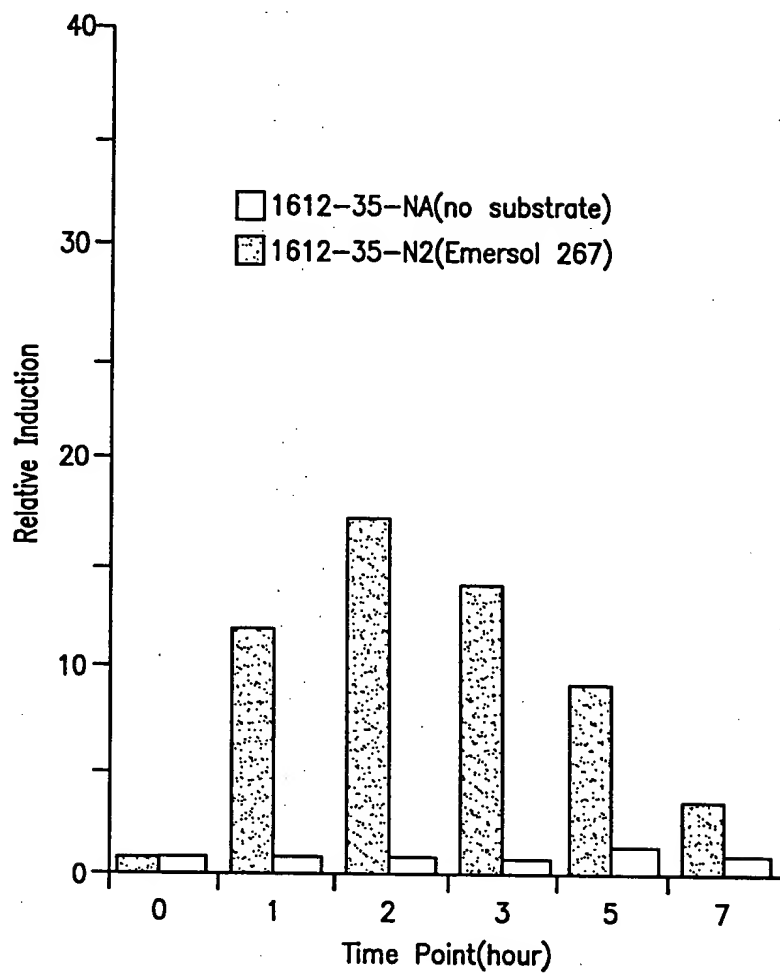


FIG. 19

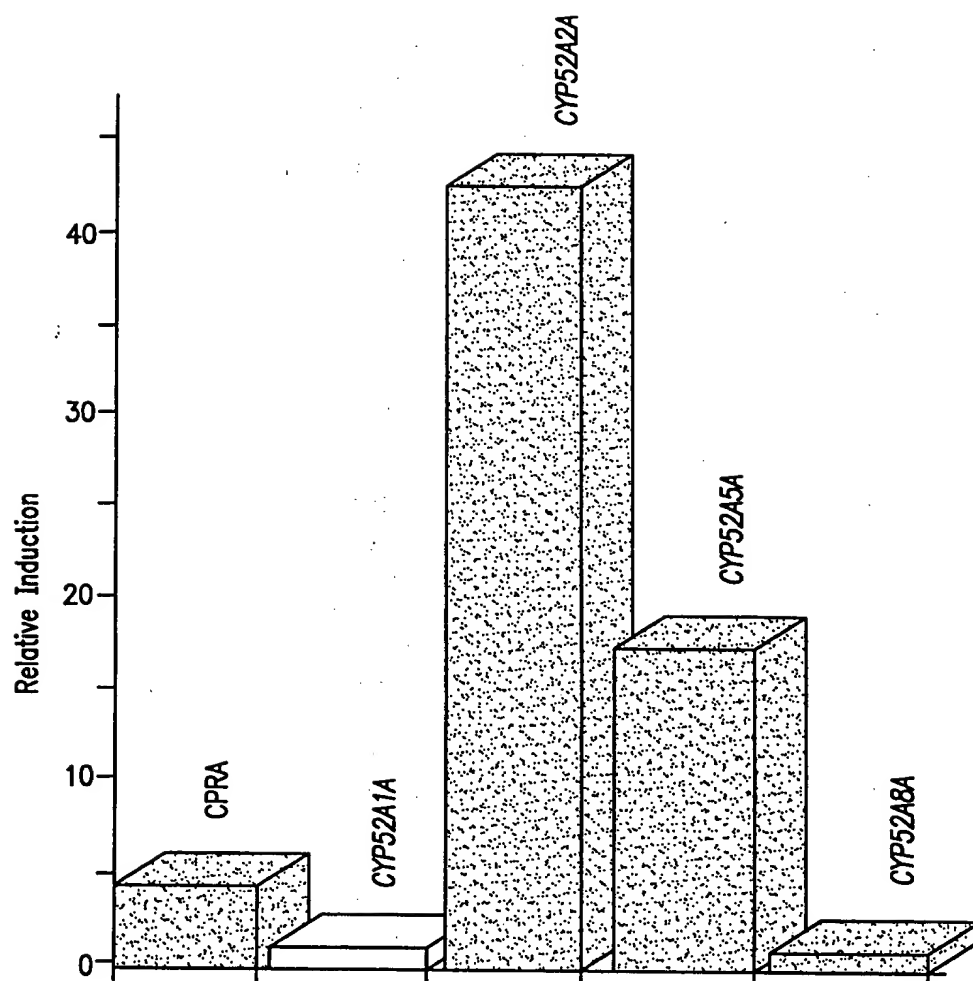


FIG. 20

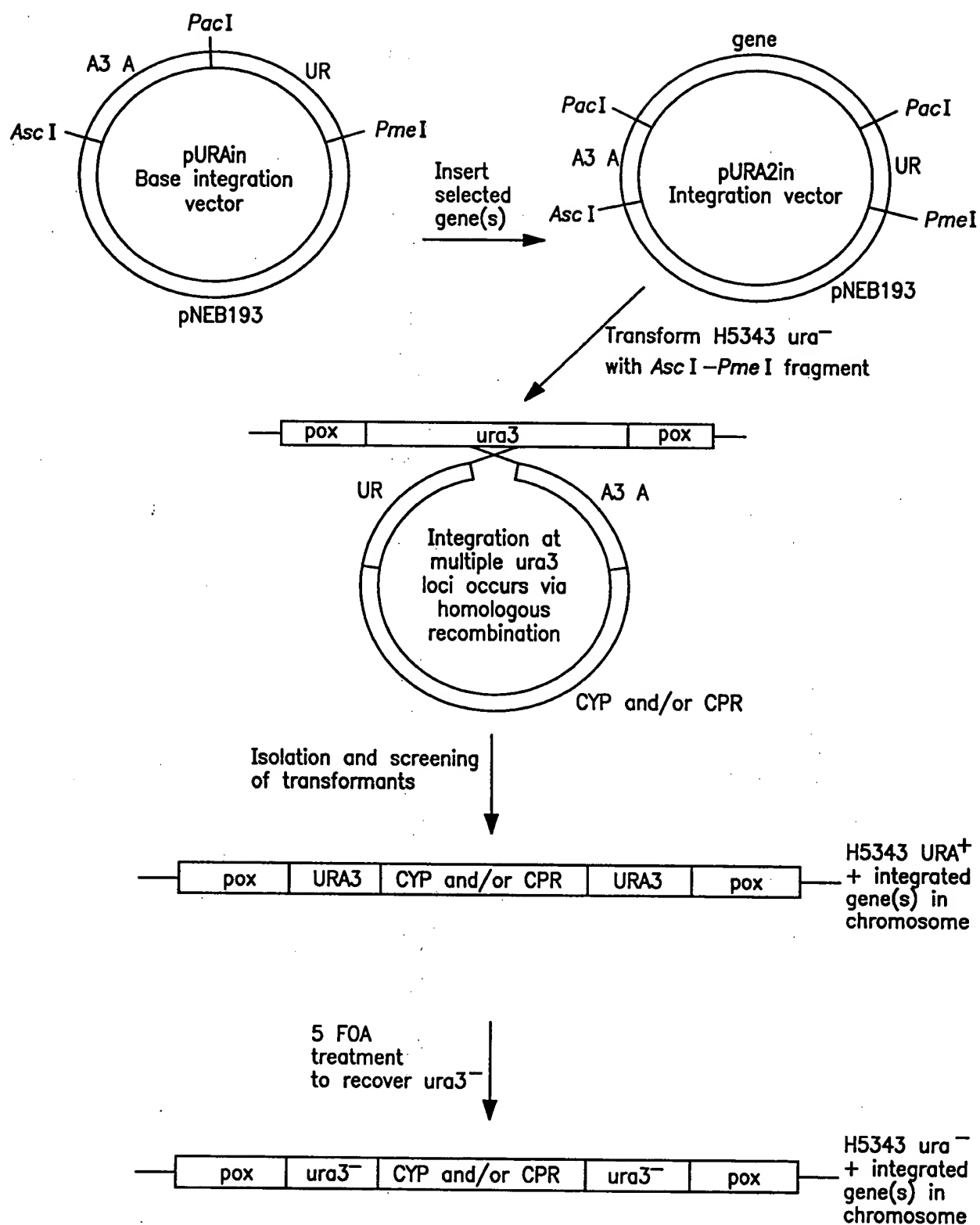


FIG. 21

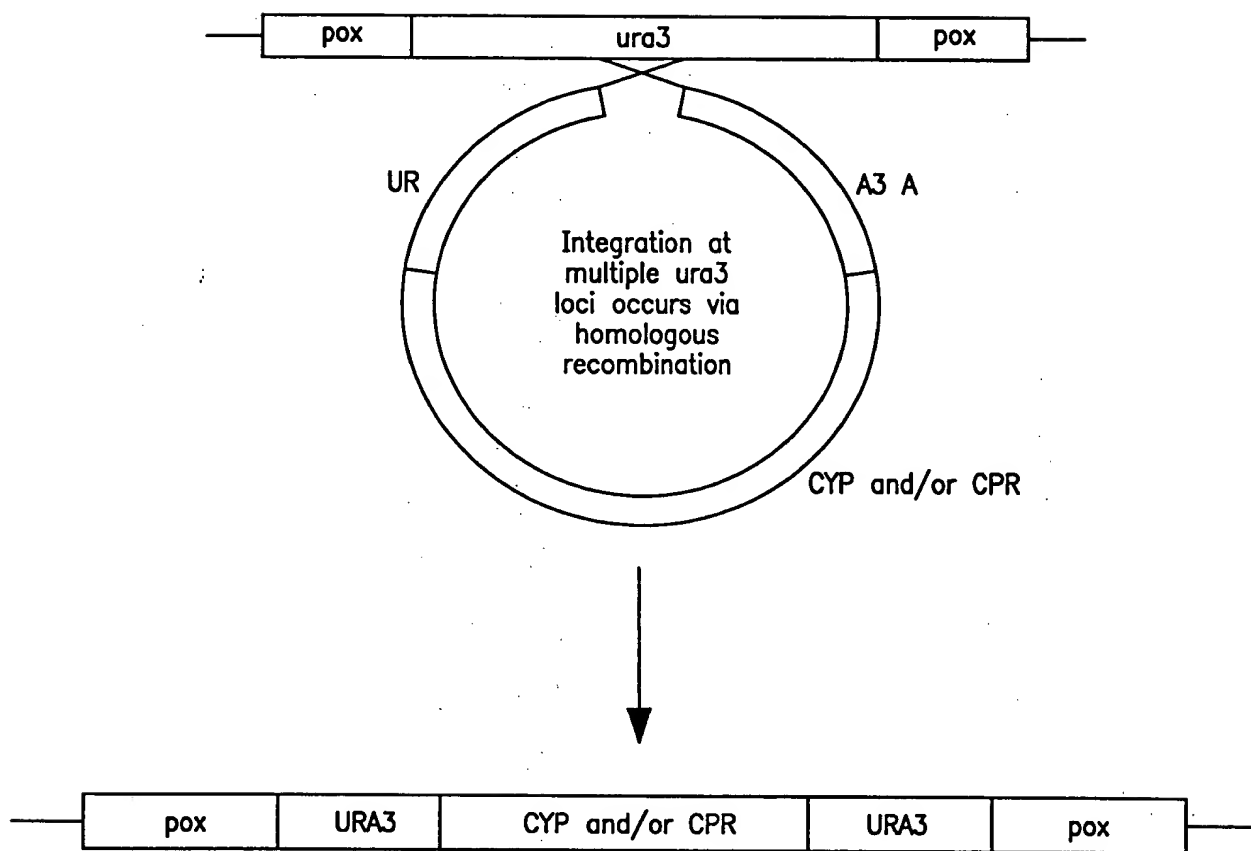


FIG. 22

Sequence Range: 1 to 1712

10	20	30	40	50	50	70	80
GGTACCGAGC	TCACGAGTTT	TGGGATTTC	GAGTTTGGAT	TGTTTCCTTT	GTTGATTGAA	TTGACGAAAC	CAGAGGTTTT
90	100	110	120	130	140	150	160
CAAGACAGAT	AAGATTGGGT	TTATCAAAAC	GCAGTTTGAA	ATATTCCAGT	TGGTTTCCAA	GATATCTTGA	AGAAGATTGA
170	180	190	200	210	220	230	240
CGATTTGAAA	TTTGAAGAAG	TGGAGAAGAT	CTGGTTTGGA	TTGTTGGAGA	ATTTCAGAA	TCTCAAGATT	TACTCTAACG
250	260	270	280	290	300	310	320
ACGGGTACAA	CGAGAATTGT	ATTGAATTGA	TCAAGAACAT	GATCTTGGTG	TTACAGAACAA	TCAAAGTTCTT	GGACCAGACT
330	340	350	360	370	380	390	400
GAGAAATGCCA	CAGATATACA	AGGCGTCATG	TGATAAAATG	GATGAGATTT	ATCCCACAAT	TGAAGAAAAGA	GTTTATGGAA
410	420	430	440	450	460	470	480
AGTGGTCAAC	CAGAAGCTAA	ACAGGAAGAA	GCAAACGAAG	AGGTGAAACA	AGAAGAAGAA	GGTAAATAAG	TATTTTGTAT
490	500	510	520	530	540	550	560
TATATAACAA	ACAAAGTAAG	GAATACAGAT	TTATACAATA	AATTGCCATA	CTAGTCACGT	GAGATATCTC	ATCCATTCCC
570	580	590	600	610	620	630	640
CAACTCCCAA	GAAAAAATAA	AAGTGAAAAA	AAAAATCAA	CCCAAAGATC	AACCTCCCCA	TCATCATCGT	CATCAAAACCC

FIG. 23A

660 660 670 680 690 700 710 720
 CCAGCTCAAT TCGCAATGGT TAGCACAAA ACATACACAG AAAGGGCATC AGCACACCCC TCCAAGGTTG CCCAACGTTT
 M V S I K T Y T E R A S A H P S K V A Q R L>

 730 740 750 760 770 780 790 800
 ATTCCGCTTA ATGGAGTCCA AAAAGACCAA CCTCTGCGCC TCGATCGACG TGACCACACAC CGCCGAGTTC CTTTCGCTCA
 F R L M E S K K T N L C A S I D V T T A E F L S L>

 810 820 830 840 850 860 870 880
 TCGACAAGCT CGGTCCCCAC ATCTGTCTCG TGAAGACGCA CATCGATATC ATCTCAGACT TCAGCTACGA GGGCACGATT
 I D K L G P H I C L V K T H I D I I S D F S Y E G T I>

 890 900 910 920 930 940 950 960
 GAGCCGTTGC TTGTGCTTGC AGAGGCCAC GGGTCTCTGA TATTCGAGGA CAGGAAGTTT GCTGATATCG GAAACACCGT
 E P L L V L A E R H G F L I F E D R K F A D I G N T V>

 970 980 990 1000 1010 1020 1030 1040
 GATGTTGCAG TACACCTCGG GGGTATACCG GATCGGCGG TGGAGTGACA TCACGAACGC GCACGGAGTG ACTGGGAAGG
 M L Q Y T S G V Y R I A A W S D I T N A H G V T G K>

 1050 1060 1070 1080 1090 1100 1110 1120
 GCGTCGTTGA AGGGTTGAAA CGCGGTGCGG AGGGGGTAGA AAAGGAAAGG GCGGTGTTGA TGTGGCGGA GTTGTGCGAGT
 G V V E G L K R G A E G V E K E R G V L M L A E L S S>

 1130 1140 1150 1160 1170 1180 1190 1200
 AAAGGCTCGT TGGCGCATGG TGAATATACC CGTGAGACGA TCGAGATTGC GAAGAGTGAT CGGGAGTTGCG TGATTGGGTT
 K G S L A H G E Y T R E T I E I A K S D R E F V I G F>

FIG. 23B

1210	1220	1230	1240	1250	1260	1270	1280
CATCGCGCAG	CGGACATGG	GGGTAGAGA	AGAAGGGTTT	GATTGGATCA	TCATGACGCC	TGGTGTGGGG	TTGGATGATA
I A Q	R D M	G G R E	E G F	D W I	I M T P	G V G	L D D>
1290	1300	1310	1320	1330	1340	1350	1360
AAGCGATGC	GTGGGCCAG	CAGTATAGGA	CTGTTGATGA	GGTGGTTCTG	ACTGGTACCG	ATGTGATTAT	TGTCGGGAGA
K G D A	L G Q	Q Y R	T V D E	V V L	T G T	D V I	I V G R>
1370	1380	1390	1400	1410	1420	1430	1440
GGGTTGTTTG	GAAAGGAAG	AGACCCTGAG	GTGGAGGGAA	AGAGATACAG	GGATGCTGGA	TGGAAGGCAT	ACTTGAAGAG
G L F	G K G R	D P E	V E G	K R Y R	D A G	W K A	Y L K R>
1450	1460	1470	1480	1490	1500	1510	1520
AACTGGTCAG	TTAGAATAAA	TATTGTAATA	AATAGGTCTA	TATACATACA	CTAAGCTTCT	AGGACGTCAT	TGTAGTCTTC
T G Q	L E	*>					
1530	1540	1550	1560	1570	1580	1590	1600
GAAGTTGTCT	GCTAGTTTAG	TTCTCATGAT	TTCGAAAACC	AATAACGCAA	TGGATGTAGC	AGGGATGGTG	GTTAGTGCCT
1610	1620	1630	1640	1650	1660	1670	1680
TCCTGACAAA	CCCAGAGTAC	GCCGCCCTCAA	ACCACGTCAC	ATTGCCCCCTT	TGCTTCATCC	GCATCACTTG	CTTGAAGGTA
1690	1700	1710					
TCCACGTACG	AGTTGTAATA	CACCTTGAAG	AA				

FIG. 23C

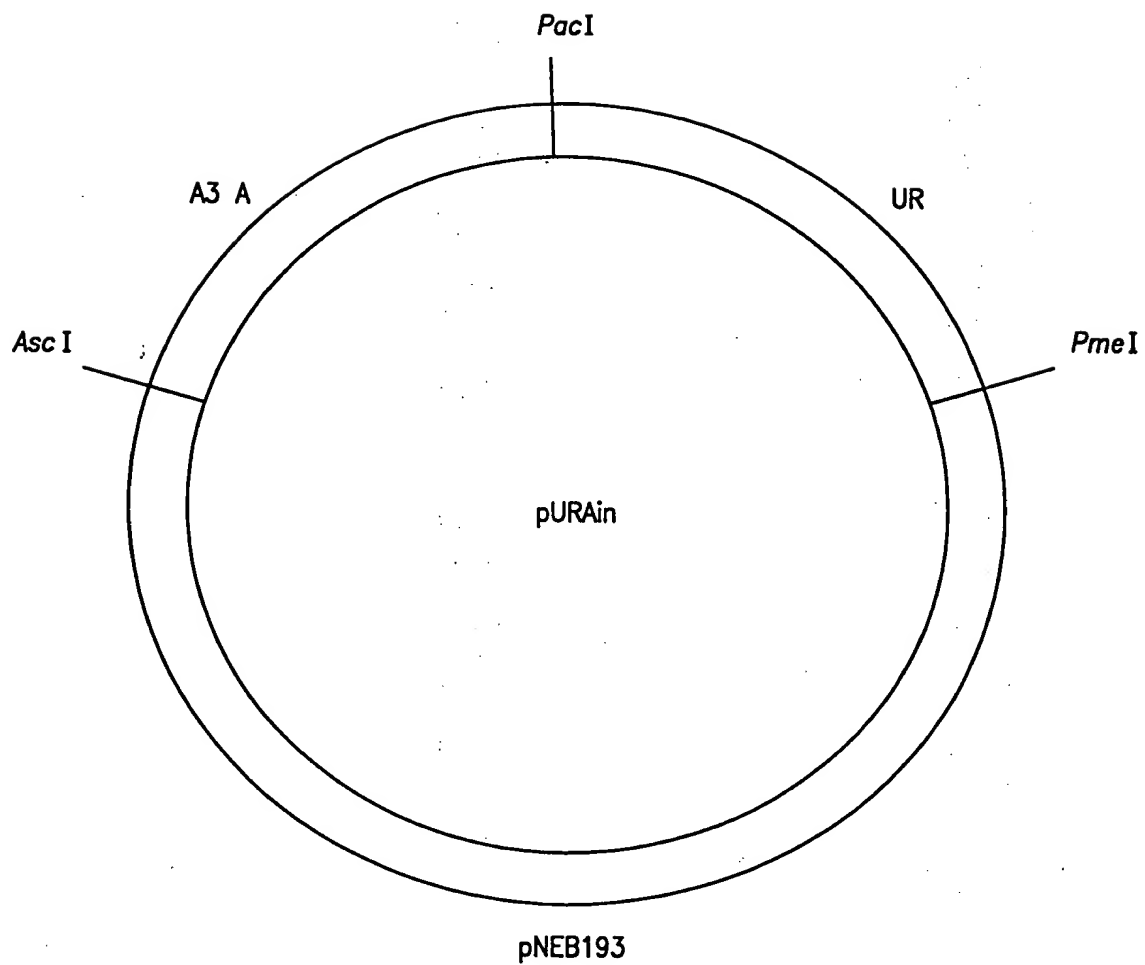


FIG. 24

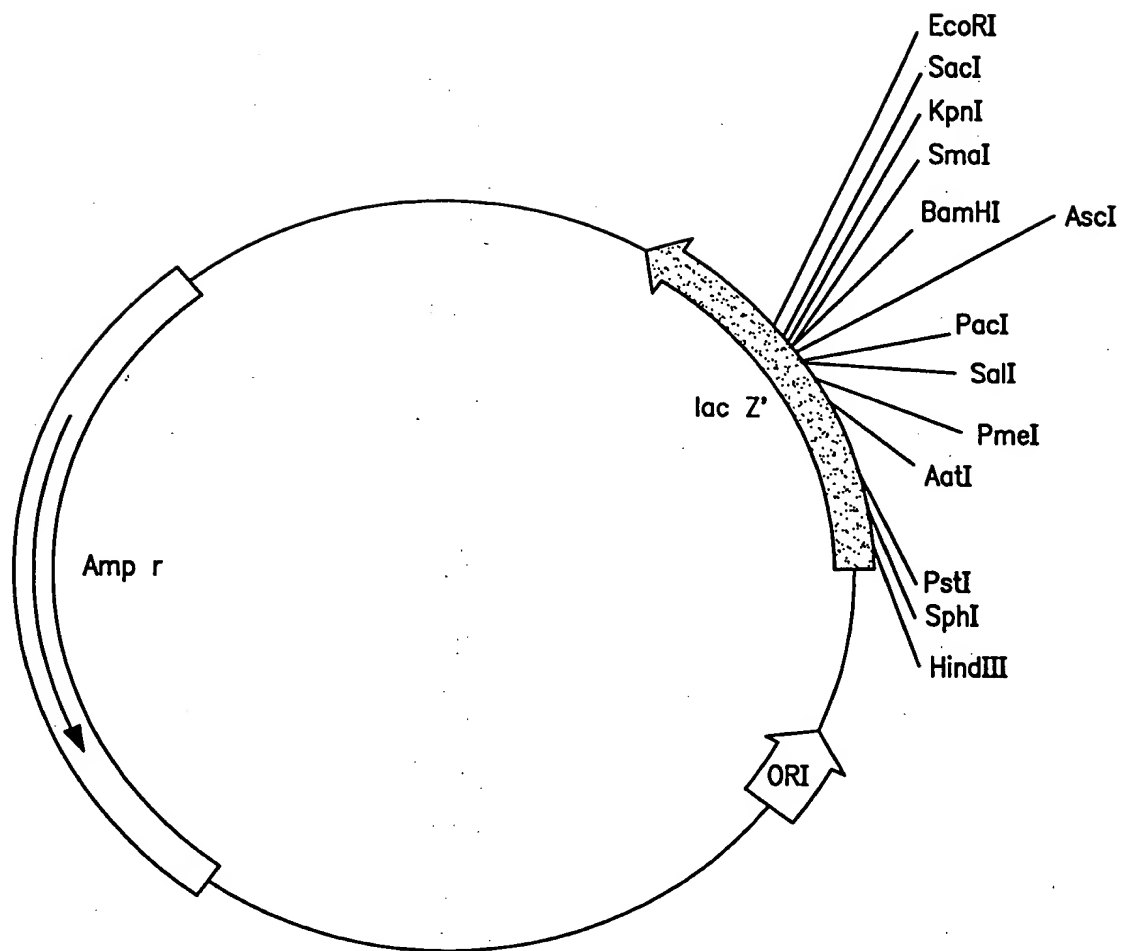


FIG. 25

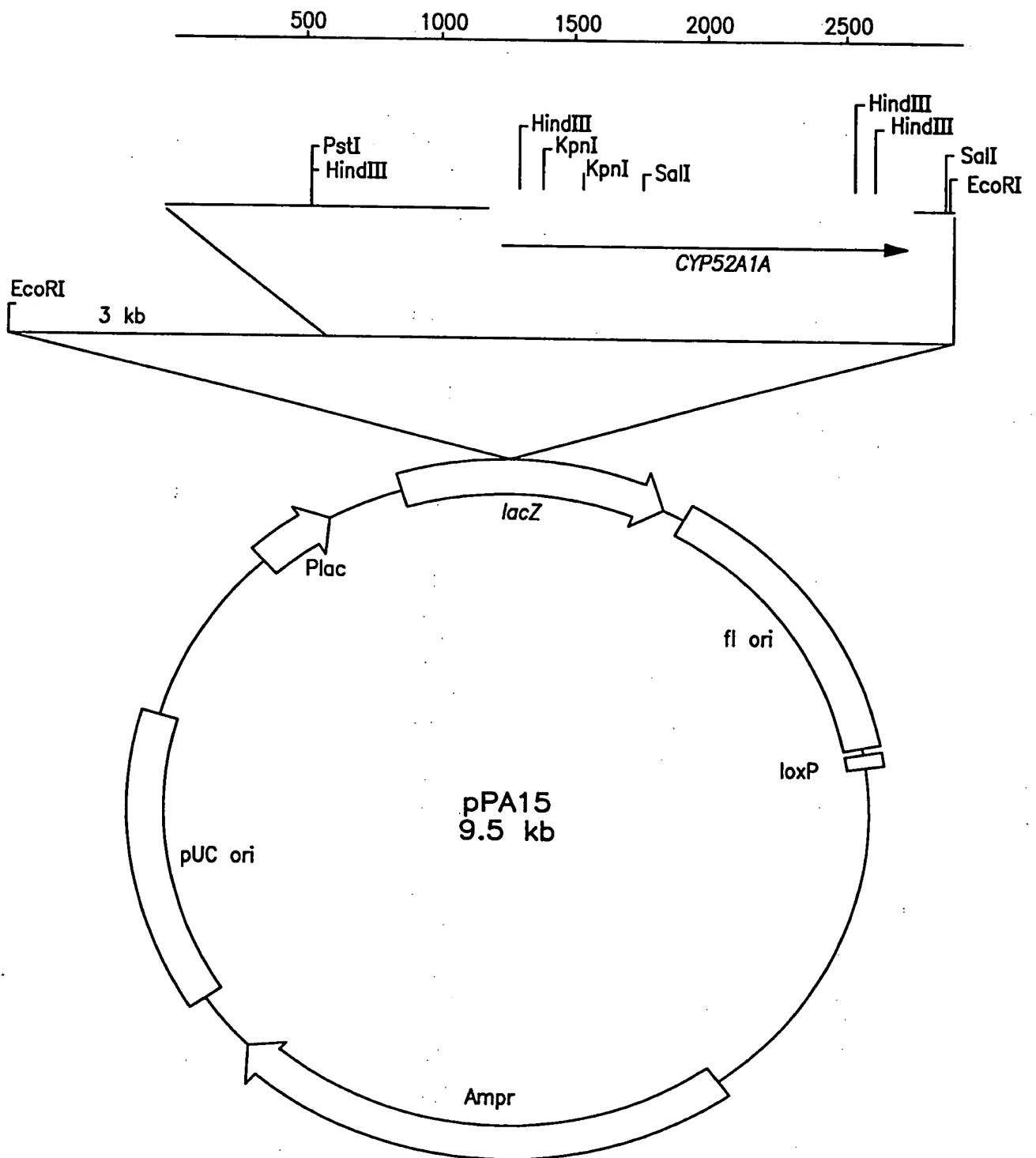


FIG. 26

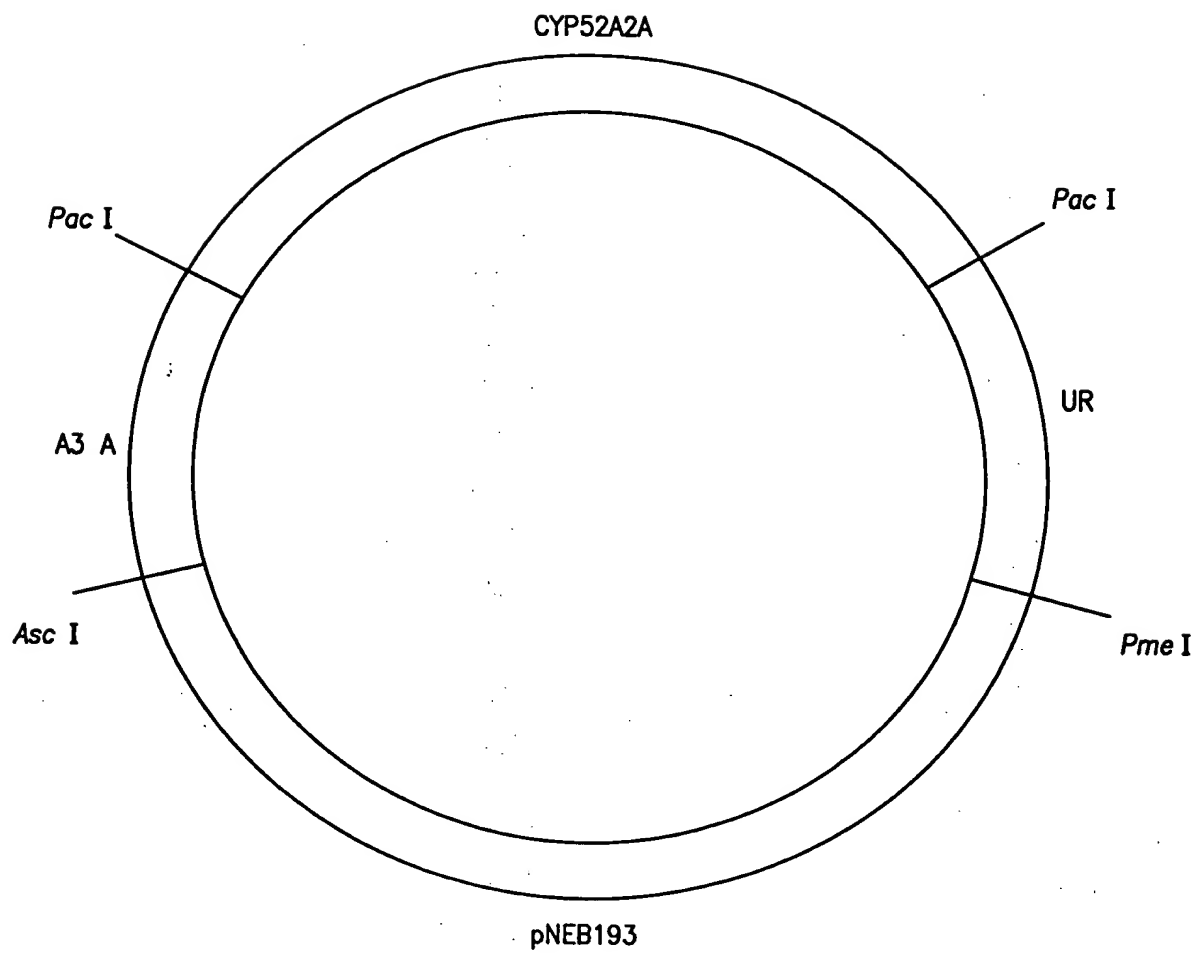


FIG. 27

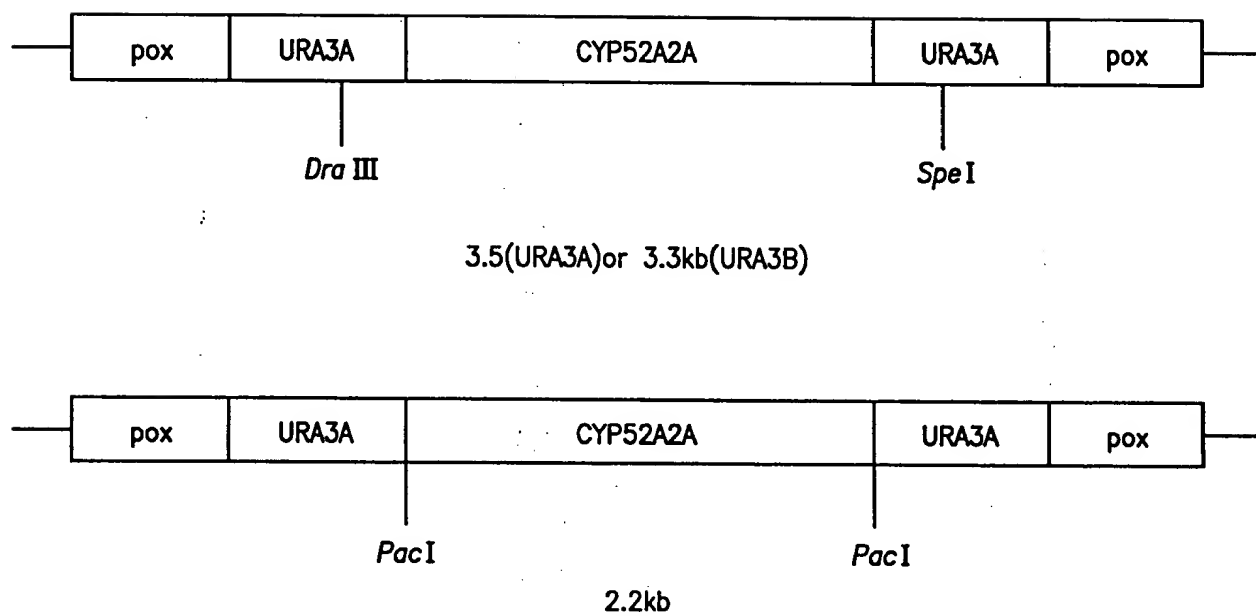


FIG. 28

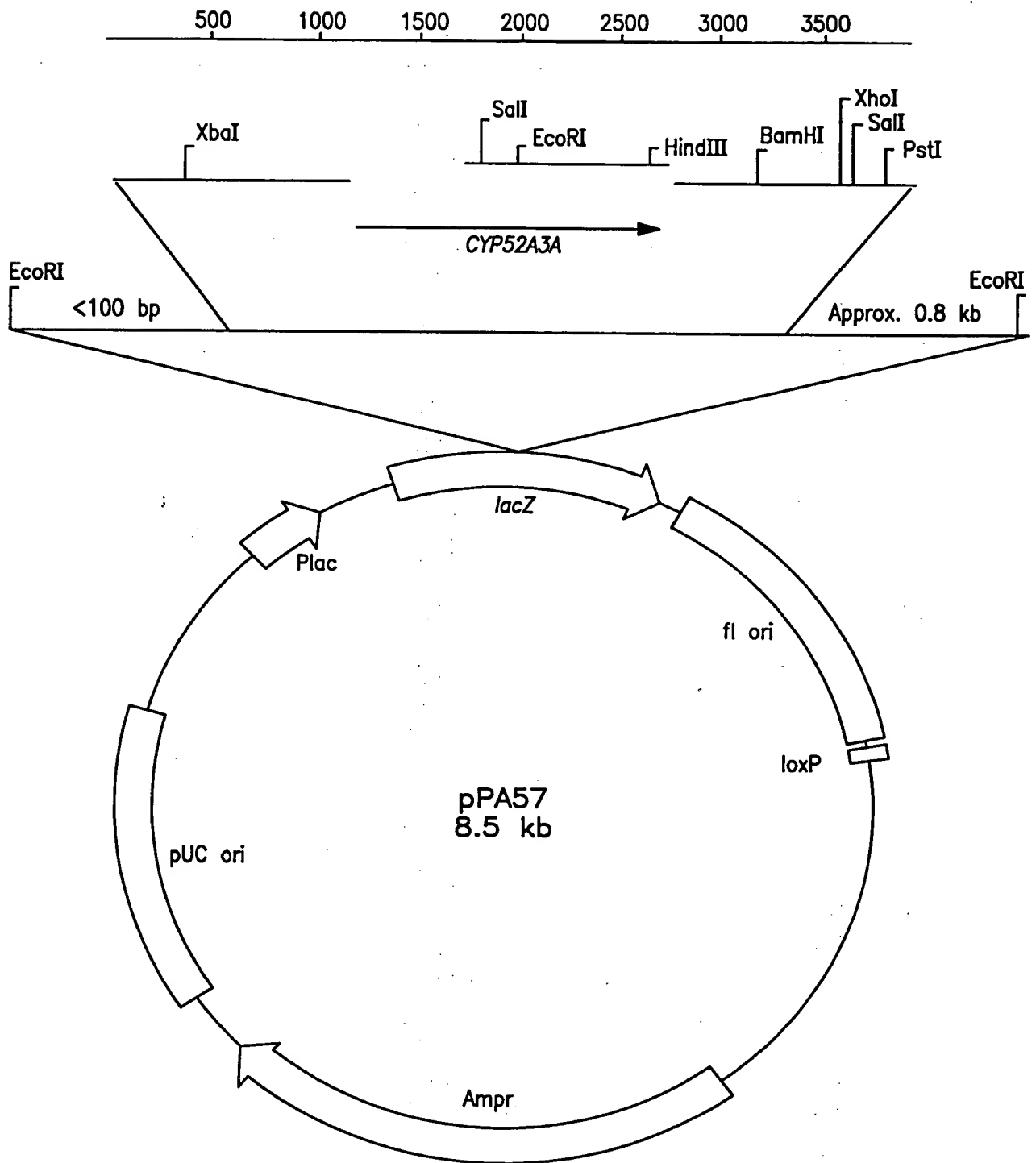


FIG. 29

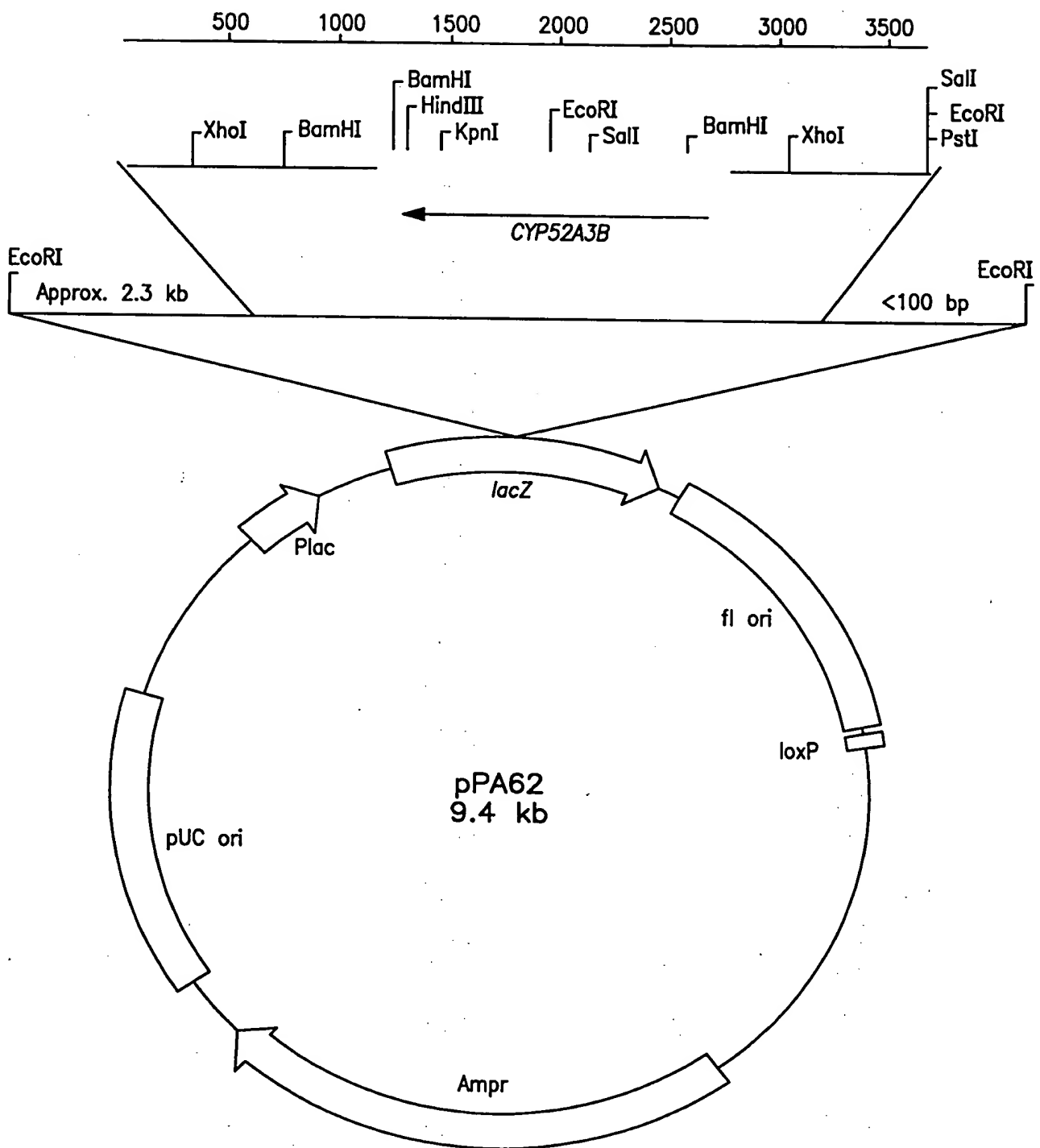


FIG. 30

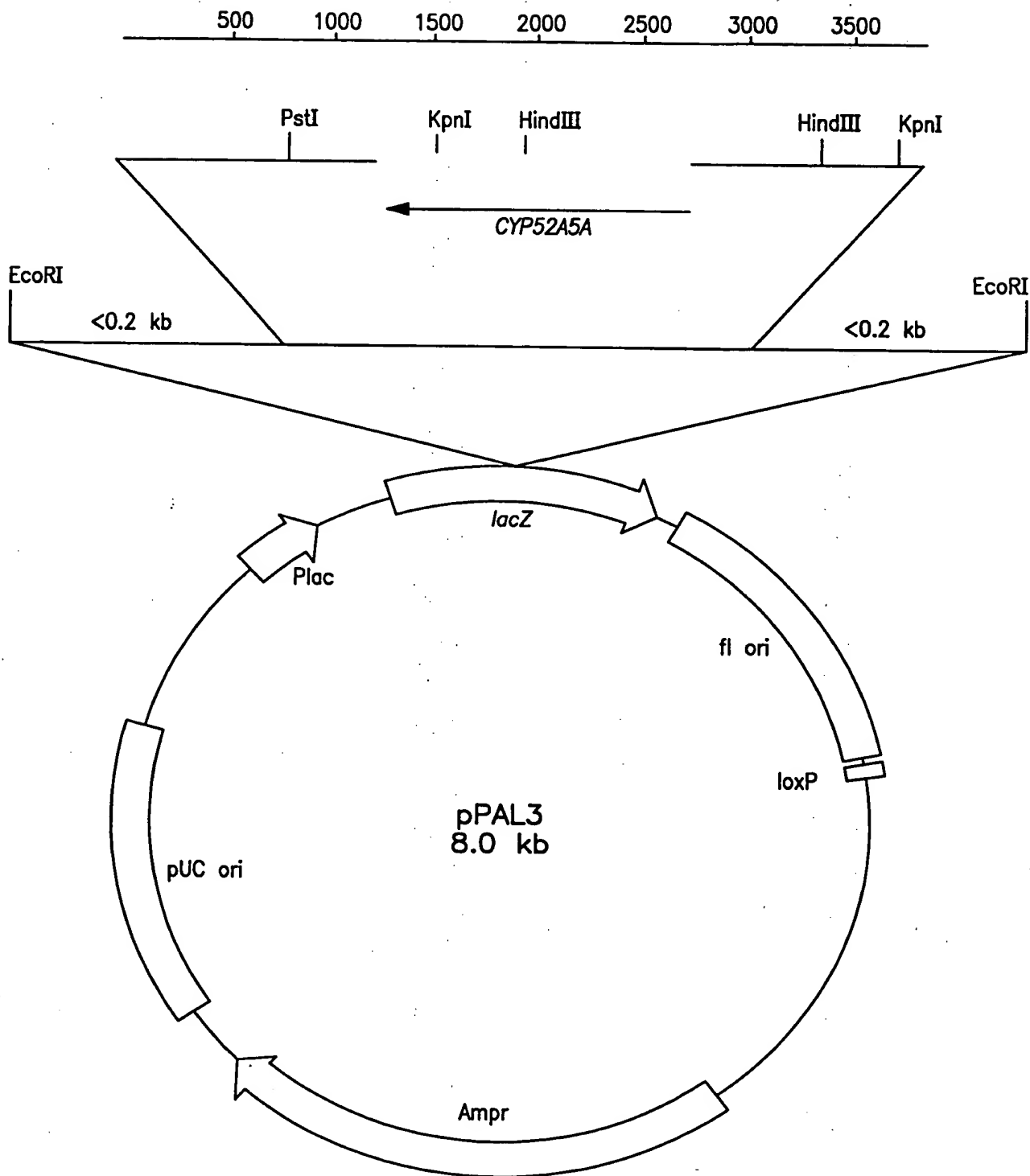


FIG. 3I

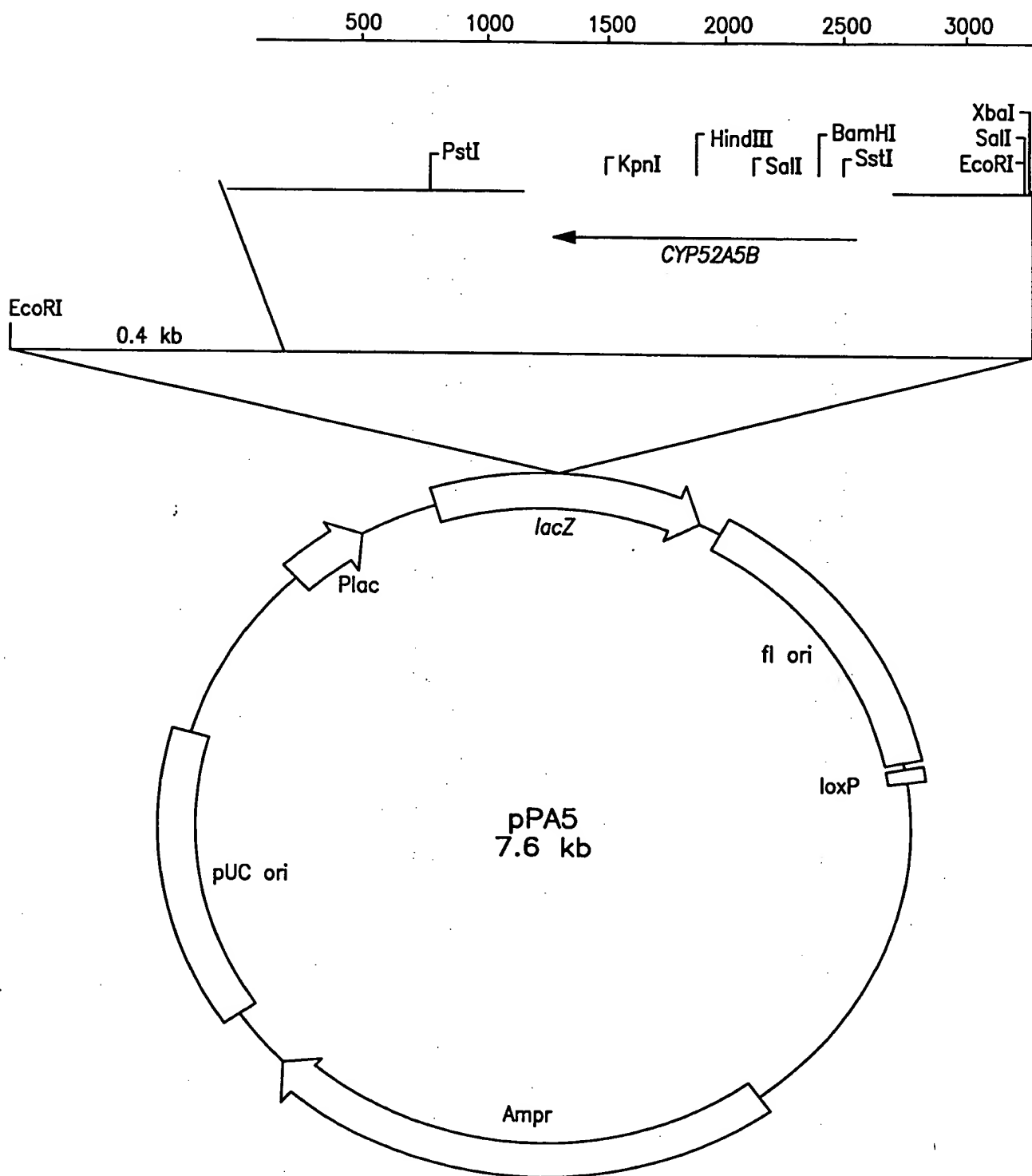


FIG. 32

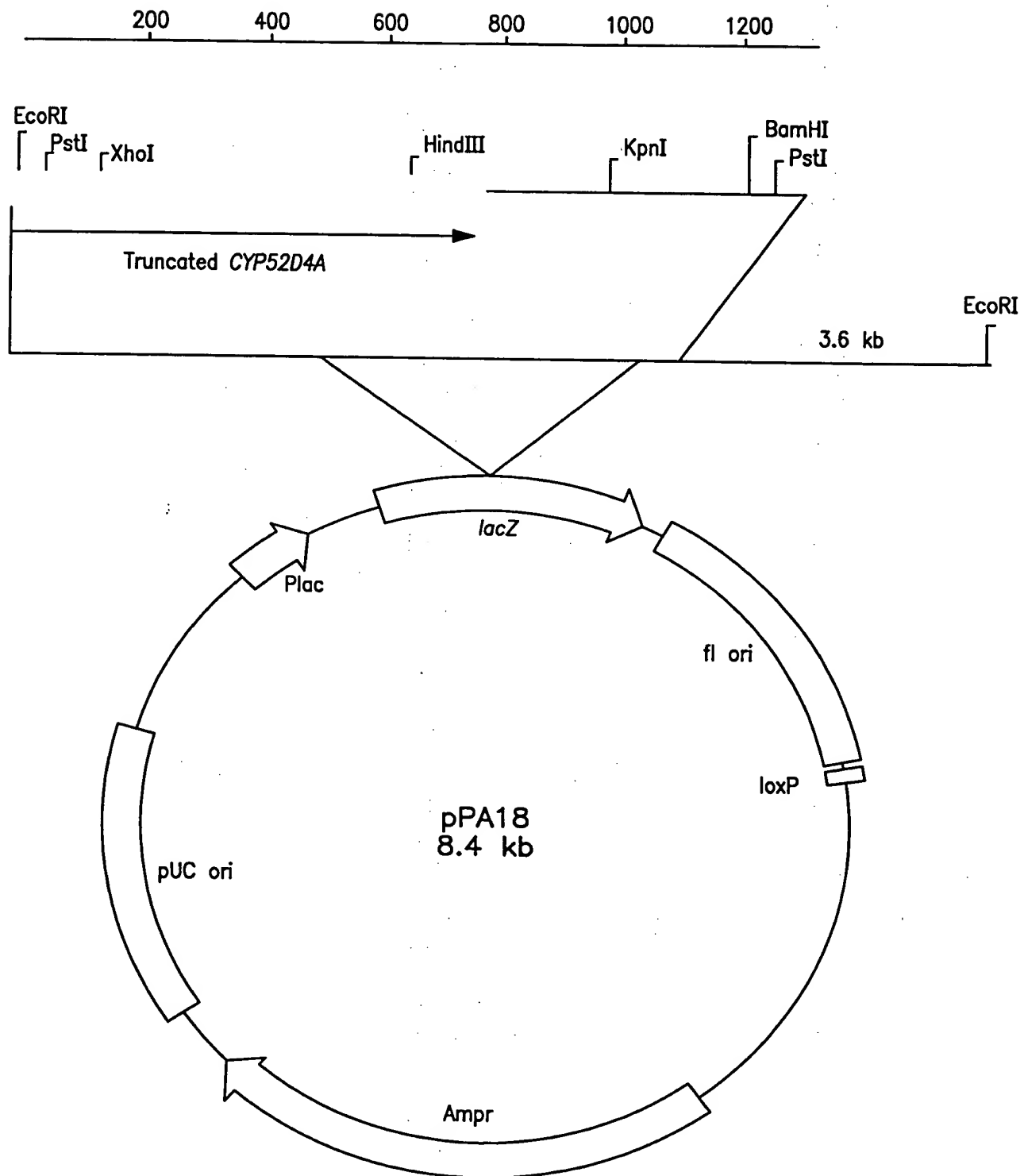


FIG. 33

Expression of CYP52A1, CYP52A2 and
CYP52A5 in Henkel Fermentor Run 3538-98

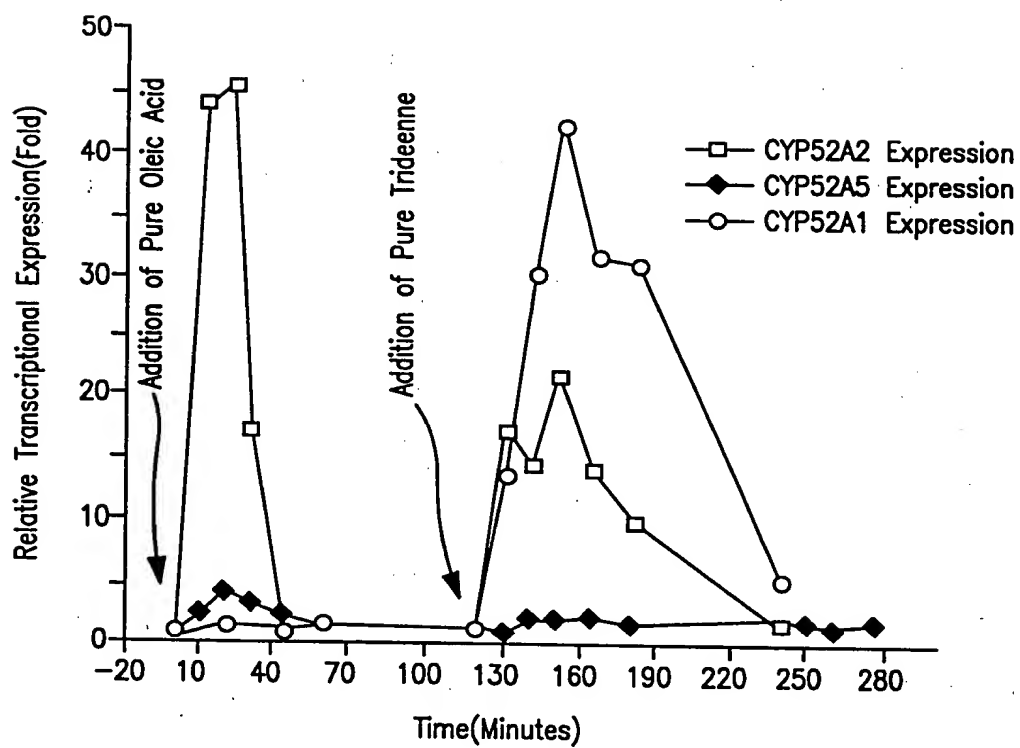
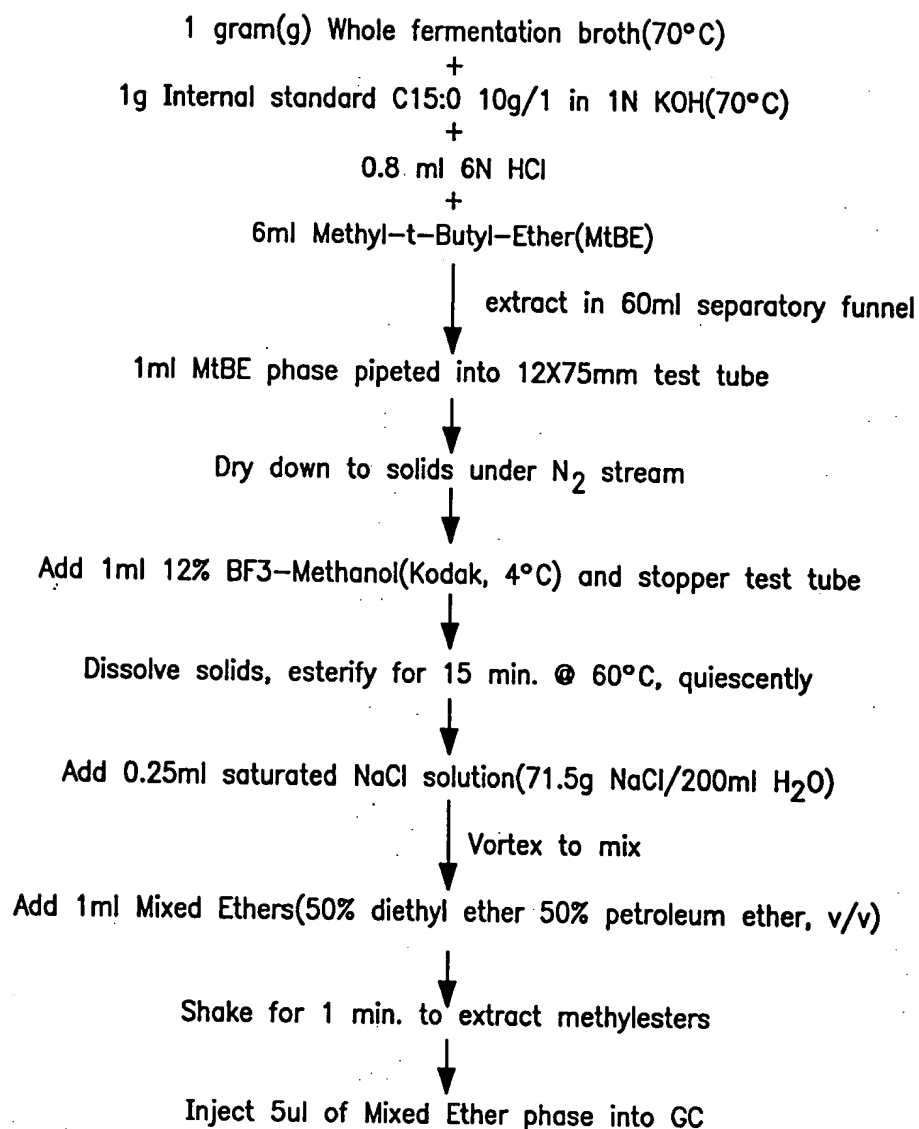


FIG. 34



GC parameters

Column : HP-INNOWAX capillary column, 30m X 0.32mm, 0.5 μ m film thickness
Split Ratio : 1:100

Column Head Pressure : 13.5 psig

Injector Temperature : 240°C

FID Detector Temp. : 250°C

Temp. Prog. : 90°C for 0 min. to 190°C @ 7°C/min. for 0 min. to 235°C @ 12°C/min. for 30 min.

FIG. 35

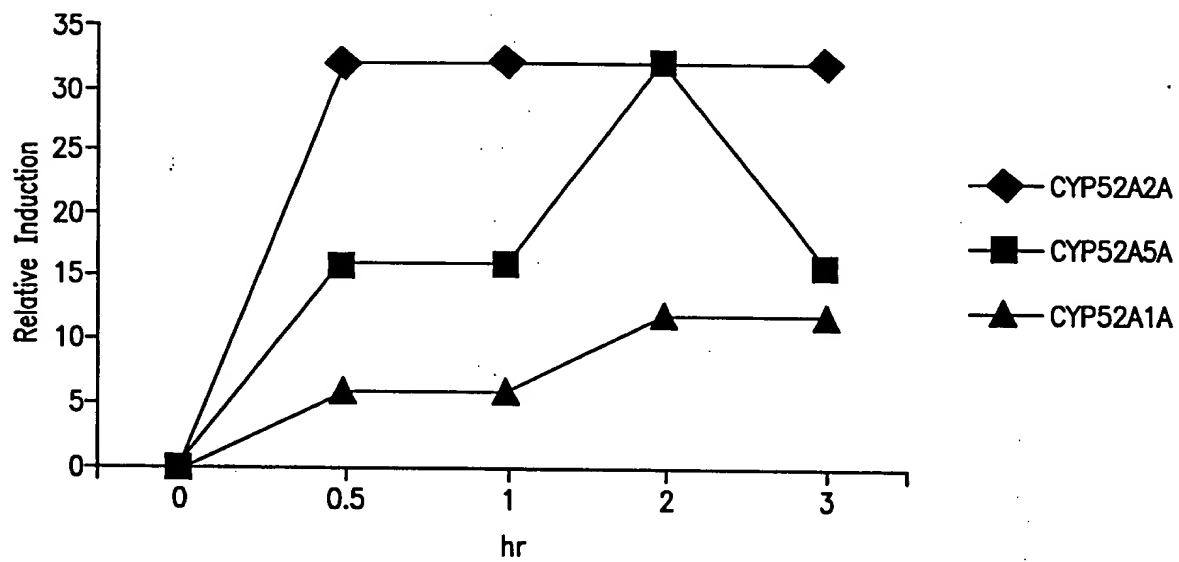


FIG. 36